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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q-cgn2_1/USPTO_Spool/US9931007/runat_14022003_102553_4678/app_query.fasta_1.839
-Q=-/cgn2_1/USPTO_Spool/US9931007/runat_14022003_102553_4678/app_query.fasta_1.839
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=bto -NORM=ext -HEAPSIZE=500 -MINEN=0 -MAXLEN=2000000000
-USER=US09931007_eCGN_1_1_3052_erunat_14022003_102553_4678 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPD=10 -XGAPD=T=0.5 -FGAPDP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0,
Delop 6.0,
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3508
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Copyright (c) 1993 - 2003 Compugen Ltd.
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29: em_vi:*
30: em_htg_inv:*
31: em_htg_other:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rdd:*
36: em_htg_rdd:*
36: em_htg_rd:*
39: em_htgo_thun:*
40: em_htgo_mus:*
41: em_htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

## No 2136.5 2196.5 2196.5 2196.5 2172.5 2177.5 2177.5 2177.5 2148.6 2148.6 2148.6 2148.6 2148.6 2148.6 2100.6 2100.6 2100.6 2100.6 2100.6 2008.6 20 Score Match Length 1008 11765 11765 11767 11768 11630 11630 11782 11782 11782 11785 1 1838 1848 2130 1428 1709 1630 1759 1428 1711 1800 1428 2089 DВ BTPPARG2 HSPPARGAM HUMPPARGB BC006811 BC006811 AF033343 AF033343 AF033343 AF048694 AY048699 AY048699 AY048699 AY048699 AY048699 AY048690 AY048690 AY048690 CGPPARGRN SSC6756 OCU84893 AF103946 SSC6757 BC021798 MMU09138 AB019561 AF156666 RNPPARGM2 AY048697 AF484684 AB045597 AF163811 HSU79012 AF033103 AY048695 AR203332 HUMPPARG AY048698 AF059245 AB011365 AF246457 AF246458 AF156665 MMU01841 MMU10374 AX409565 Sequence AR13920 Sequence AR030509 Sequence AB011365 Rattus no AF246457 Rattus no AF246458 Rattus no AF15665 Rattus no U01841 Mus musculu U10374 Mus musculu U30972 C.griseus m AJ006756 Sus scrof AY048698 Macaca fa AF059245 Sus scrof AF103946 Sus scrof AJ006757 Sus scrof BC021798 Mus muscul U09138 Mus muscul AB019561 Rattus no AF156666 Rattus no Y12882 Rattus norv AY048697 Macaca fa X90563 H.Sapiens m L40904 Homo Sapien BC006811 Homo Sapien BC006811 Homo Sapien AF033342 Macaca mu AF033342 Macaca mu AF033342 Macaca fa AY048694 Macaca fa AY048696 Macaca fa AY048696 Macaca fa U84893 Oryctolagus AF317514 Cavia por Y12419 B.taurus mR AF484684 Anas plat AB045597 Gallus ga AF163811 Gallus ga U63415 Human perox AR121467 Sequence D83233 Homo sapien AF033103 Macaca U79012 Human ligan Description U01664 Mus musculu Sequence

ALIGNMENTS

379 LeuLeuGlnAl	Qy	81 IleProPheThrArgThrAspProValValAlaAspTyrLysTyrAspLeuLysLeuGln 100	Qy
	Db	61 ASPIleLysProPheThrThrValAspPheSerSerIleSerThrProHisTyrGluAsp 80 	Qy Db
1201 AAGTTCAATGC	o dd .	41 ThrasnPheGlyIleSerSerValAspLeuSerValMetGluAspHisSerHisSerPhe 60 	Qy Db
1141 CTAAAGAGCCT	0 D K	21 LeuSerAlaAsnIleSerGlnGluMetThrMetValAspThrGluMetProPheTrpPro 40 	Qу
	0 dd x	1 MetGlyGluThrLeuGlyAspSerProIleAspProGluSerAspSerPheThrAspThr 20 	Qy Db
1021 GACCAAGIAAC	2 5	-09-931-007A-1 (1-688) x HSU63415 (1-1518)	US-09
	Qy	Query Match:       63.60%       Indels:       62         DB:       9       Gaps:       1	Query DB:
259 ValGlnGluIl           961 GTGCAGGAGAT	Qy Db	1.32e-159 Length: 2231.00 Matches: 87.72% Conservative: 87.728 Mismatches:	Pred. Score: Percen Best L
901 CAGAGCAAAGA	Db	1	ORIGI
239 GlnSerLysGl	Qy	OUNT 438 a	BASE CO
	Db	VNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFM EPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK	
219 AsnSerLeuMe	Qy	EKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFV IYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGF	
199 AlaArgAlaIl              781 GCGAGGGCGAT	Qy dd	ISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEY QSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCK GFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEK	
	Db	/protein_id="AAB04028.1" /db_xref="G1:1432177" /translation="MGETLODSPIDPESDSFTDTLSANISOEMTMYDTEMPTNFG	
	Ωу , 1	/product="peroxisome proliferator activated receptor gamma $2$ "	
159 LeuLeuAlaG1             661 CTGTTGGCGGA	Оу	CDS . 1.1518 /codon_start=1	
0	Db	/organism="Homo sapiens" /db_xref="taxon:9606"	
	Qy	FEATURES Location/Qualifiers source 11518	FEATU
541 CGGATCCACAA	Db	AL	nor
125	Qy		TT TT
481 GGTTTCTTCCG	ρb	AUTHORS Elbracht A Chan V Cullinan C A Haves N Lebruitz M D AUTHORS Elbracht A Chan V Cullinan C A Haves N Lebruitz M D	REFER
	Qy		TIT
421 GTCTGTGGAGA	Db	<pre>Moller,D.E. and Berger,J.</pre>	AUT
124	Qy	REFERENCE 1 (bases 1 to 1518)	REFER
121 GlnLeuTyrAs	Db	NISM Hon	ORGA
	Db	SC	VERSI KEYWO
101 GluTyrGlnSe	Qy	complete cds. U63415	ACCES
241 ATTCCATTCAC	Db	415 HSU63415 TOTION Himan peroxisome proliferator activated recentor gamma 2	HSU63

	Qy 121 GlnLeuTyrAsn	Qy 101 GluTyrGlnSerAlaIleLysValGluProAlaSerProProTyrTyrSerGluLysThr 120 	Oy 81 IleProPheThrArgThrAspProValValAlaAspTyrLysTyrAspLeuLysLeuGln 100 	Qy 61 AspileLysProPheThrThrValAspPheSerSerIleSerThrProHisTyrGluAsp 80	ThrasnPheGlyIleSerSerValaspLeuSerValMetGluaspHisSerHisSerPhe	21 LeuSerAlaasnIleSerGlnGluMetThrMetValAspThrGluMetProPheTrpPro 40 	1 MetGlyGluThrLeuGlyAspSerPr 	/ Match: 63.60% Indels: 63.60% Gaps: 63.60% (1-668)	No.: nt Si Local	BASE COUNT 462 a 380 c 361 g 405 t ORIGIN Alignment Scores	JOURNAL PATENT: US 6159734-A 3 12-DEC-2000; FEATURES Location/Qualifiers Source 1. 1608 Vorganisms" unknown"	REFERENCE 1 (bases 1 to 1608) AUTHORS McKay,R., Borchers,A.H. and Baker,B.F. TITLE Annua expression amma expression	S Unknown. ISM Unknown. Unclassified.	LOCUS AR121467 1608 bp DNA linear PAT 16-MAY-2001 DEFINITION Sequence 3 from patent US 6159734. ACCESSION AR121467.1 GI:14105043	Db 1501 TACAAGGACTTGTAC 1515  RESULT 2  AR121467	Qy 439 TyrLysAspLeuTyr 443	Qy 419 LeuGlnValIleLysLysThrGluThrAspMetSerLeuHisProLeuLeuGlnGluIle 438	1381 GCCAAGCTGCTCCAGAAAATGACAGACCTCAGACAGATTGTCACGGAACACGTGCAGCTA	Db 1321 CTGCTACAAGCCCTGGAGCTCCAGCTGAAGCTGAACCACCCTGAGTCCTCACAGCTGTTT 1380
Qy	Db	70 40 70	Db Qy	o by	Qy Db	Qy Db	Qу	Qy Db	Qу	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	ρb	Д Ду	Qy	Dy Oy
439 TyrLysAspLeuTyr 443	CTGCAGGTGATCAAGAAGACGGAGACATGAGTCTTCACCCGCTCCTGCAGGAGATC 15	Ledus Linysmetrini Aspleedai Gs.ini.Levali Tilosini Isvatorin Levali Tilosini Symetrini Aspleedai Gs.ini.Levali Tilosini Statorin Levali Tilosin Levali Tilosini Statorin Levali Tilosini Statorin Levali Tilosini Statorin Levali Tilosin Levali Ti	LeuteuG.InAtaleuGtüleuGinleulysteuksnHisProGlüserSerGinleuPhe 39	LeuSerGlyAspArgProGlyLeuLeuAsnValLysProTleGlnAsp1LeGlnAspAsn	9 LysPheAsnAlaLeuGluLeuAspAspSerAspLeuAlaIlePheIleAlaValIleIle 35	319 LeuLysSerLeuArgLysProPheGlyAspPheMetGluProLysPheGluPheAlaVal 338 	299 LeuMetAsnLysaspGlyValLeuIleSerGluGlyGlnGlyPheMetThrargGluPhe 318 	279 ASPGInValThrLeuLeuLysTyrGlyValHiSGluIleIleTyrThrMetLeuAlaSer 298	259 ValGlnGluIleThrGluTyrAlalysSerIleDroGlyPheValAsnLeuAspLeuAsn 278 	239 GlnSerLysGluVaiAlaTleArgTlePheGlnGlyCysGlnPheArgSerValGluAla 258 	219 AsnSerLeuMetMetGlyGluAspLysIleLysPheLysHisIleThrProLeuGlnGlu 238 	199 AlaArgAlaIleLeuThrGlyLysThrThrAspLysSerProPheValIleTyrAspMet 218 	179 AlaLeuAlaLysHisLeuTyrAspSerTyrIleLysSerPheProLeuThrLysAlaLys 198 	159 LeuLeuAlaGluIleSerSerAspIleAspGlnLeuAsnProGluSerAlaAspLeuArg 178 	139 ValGiyMetSerHisAsnalaIleArgPheGlyArgMetProGlnAlaGluLysGluLys 158 	631 CGGATCCACAAAAAAGTAGAAATAAATGTCAGTACTGTCGGTTTCAGAAATGCCTTGCA 690	GATTGAAGCTTATCTATGACAGATGTGATCTTAACTG snLysCysGlnTyrCysArgPheGlnLysCysLeuAl	124 124	24 1 11 OROMONIO NAVINANO NOTATION NAVINANO NAVINAN

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Best Local Similarity:
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TITLE
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                           TACAAGGACTTGTAC 1605
 {\tt ThrAsnPheGlyIleSerSerValAspLeuSerValMetGluAspHisSerHisSerPhe}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (20-NOV-1996) Cardiovascular Research,
Pharmaceuticals, Inc., 9393 Towne Centre Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9065481
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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GKLAEISSDIDQLMPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFV
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PPARgamma2"
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                                                                                                             LeuMetAsnLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPhe 318
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BASE CO	FEATURES SOUR gene	AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Db 1591 RESULT 4 AF033103 LOCUS DEFINITION ACCESSION VERSION V		Db 1291 Qy 359 Db 1351 Qy 379 Db 1411
/codon_start=1 /product="peroxisome proliferator-activated receptor gamma /product="peroxisome proliferator-activated receptor gamma /protein_id="AAB87480.1" /db_xref="gi:2645731" /db_xref="gi:26457	e rce	Hotta,K., and Hanses Relations; Relations; and hyper; Unpublish 2 (Dases Hotta,K., and Hanses Direct Sul Submitted Maryland, Baltimore	#13 TILLYSHSPLEUTYI	AlaLysLeuLeuGlnLysMetThrAspLeuArgGlnIleValThrGluHisValGlnLeu	1291 AAGTTCAATGCACTGGAATTAGATGACAGCGACTTGGCAATATTTATT
Db 685 CTGTTGGCGGAGATCTCCAGTGATTGGACCAGAGTCCACGAGTCCCGG 744  Qy 179 AlaLeuAlaLysHisLeuTyrAspSerTyrIleLysSerPheProLeuThrLysAlaLys 198	Qy 125	121 GINLEUTYFASN	Oy  41 ThrasnPheGlyIleSerSerValAspLeuSerValMetGluAspHisSerHisSerPhe 60  141 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	09-931-007A-1 (1-688) x AF033103 (1-1759)  1 MetGlyGluThrLeuGlyAspSerProIleAspProGluSerAspSerPheThrAspThr	ORIGIN  Alignment Scores:  Pred. No.:  217.00  Percent Similarity:  Best Local Similarity:  86.118  Query Match:  63.208  Length:  1759  Matches:  40  Conservative:  5  Lindels:  62  Gaps:  1

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                                                              Direct Submission
Submitted (27-JUL-2001) Internal Medicine,
200 Hawkins Drive, Iowa, IA 52242, USA
                                                                                                                                                       Zhou,J., Wilson,K.M. and Medh,J.D. Genetic analysis of four novel per receptor-gamma splice variants in Biochem. Biophys. Res. Commun. 293
                                                                                                     2 (bases 1 to 1765)
Zhou, J., Wilson, K.M.
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in monkey macrophages
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                                                                           GGTTTCTTCCGGAGAACAATCAGATTGAAGCTTATCTATGACAGATGTGATCTTAACTGT
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CAGGCCCTGGCAAAACATTTGTATGACTCATACATAAAGTCCTTCCCGCTGACCAAAGCA
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                                                        PPAR gamma2
Unpublished
2 (bases 1
Direct Submission
Submitted (29-JAN-1996) Shigeaki Kato, Tokyo University of Agriculture, Department of Agricultural Chemistry; Sakuragaoka 1-1-1, Setagaya-ku, Tokyo 156, Japan (E-mail:ktake@m.u-tokyo.ac.jp, Tel:03-5477-2318, Fax:03-5477-2619)
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CAGCTCTACAATAAGCCTCATGAAGAGCCTTCCAACTCCCTCATGGCAATTGAATGTCGT
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                                                                                                                                      GTCTGTGGAGATAAAGCTTCTGGATTTCACTATGGAGTTCATGCTTGTGAAGGATGCAAG
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405 c 377 g 420 t
ArgAsnLysCysGlnTyrCysArgPheGlnLysCysLeuAla
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Cercopithecidae;

Euteleostomi;

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                                                   proliferator-activated
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Best Local Similarity:
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AspThrGluMetProPheTrpProThrAsnPheGlyIleSerSerValAspLeuSerVal
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                                                 GACACAGAGATGCCATTCTGGCCCACCAACTTTGGGATCAGCTCCGTGGATCTCTCCGTA
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Direct Submission
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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1 (bases 1 to 1849)
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DGVFISGGQGFMTREFLKSLRKPFGDFMEPKFEFAVKEVALELDDSDLAIFIAVIILS
GDRPGLLNVKPIEDIQDNLLQALELGKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
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3 437 c 396 g 462 t
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OYCRFOKCTAVGMSHARITTGKTTDKSPPYIYDMNSLAMGEDKIKFKHITPLOEOSKEVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Macaca fascicularis"
/db_xref="taxon:9541"
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Catarrhini; Cercopith
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Sus scrofa
Eukaryota;
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Submitted (13-APR-1998) Animal
Poultry Science Building, West
Location/Qualifiers
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(PPARG) mRNA,
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FFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCREPQKCLAVGMSHNAIRFGRMPQAEKE
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Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Su;

1 (bases 1 to 1539)

RS Ding,S.T., McNeel,R.L. and Mersmann,H.J.

Expression of porcine adipocyte transcripts: tissue di
and differentiation in vitro and in vivo

comp. Biochem. Physiol. B, Biochem. Mol. Biol. 123 (3)
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Ding, S.T. and Mersmann, H.J.
Direct Submission
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/product="peroxisome I
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Qy 101 c	Qy 81 1 Db 298 <i>i</i>	Qy 61 <i>I</i> Db 238 (	Qy 41 7 Db 178 <i>I</i>	Qy 21 I Db 118 (	Qy 1 N Db 61 <i>I</i>	US-09-931-(	Query Match:	Pred. No.: Score: Percent Sir	ORIGIN Alignment	BACE COUNT						CDS	gene		FEATURES Source	MEDLINE	TANALIOT	AUTHORS TITLE	REFERENCE	AUTHORS TITLE
GluTyrGlnSerAlaIleLysValGluProAlaSerProProTyrTyrSerGluLysThr 120 :::	TleProPheThrArgThrAspProValValAlaAspTyrLysTyrAspLeuLysLeuGln 100 	ASPI1eLysProPheThrThrValAspPheSerSerI1eSerThrProHisTyrGluAsp 80	ThrasnPheGlyIleSerSerValaspLeuSerValMetGluaspHisSerHisSerPhe 60	LeuSerAlaAsnIleSerGlnGluMetThrMetValAspThrGluMetProPheTrpPro 40 	MetGlyGluThrLeuGlyAspSerProIleAspProGluSerAspSerPheThrAspThr 20 	x SSC6757 (1-1640)	dilitarity: 03.136 mismatches: 61.598 Indels: 4 Game:	3.03e-154 2160.50 ty: 86.53%	SCOLDS:	PKFEFAVKFNALELDDSDLAII NHPESSQLFAKLLQKMTDLRQI	KLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVI YDMNSLMMGEDKIKFKHITTPLOEOSKEVAIRIFOGCOFRSVEAVQEITEYAKNIPGFV	SSVDLSVMDDHSHSFDIKPFTTVDFSSISTPHYEDIPFPRADPMVADYKYDLKLQDYQ SAIKVEPVSPYYSEKTQLYNKPHEEPSUSLAALECRVCGDKASGFHYGYHACEGCKG FFRRTIRKLLIYDRODLNCFIKKKSRNKOOYCRFOKCLAVGMSHANIRFGRMPOAFKF	/protein_id="CAA07225.1" /db_xref="GI:3646470" /db_xref="SPTREMBL:077815" /translation="MGEFIGDSLIDPESDAFDTLSANISOFVTMYDTEMPEWPTNEGI	/product="peroxisome proliferator-activated receptor-gamma/product="peroxisome proliferator-activated receptor-gamma/"	/function="adipocyte differentiation, fat deposition, regulation of adipogenesis" /codon start=1	/gene="PPARg2"	/cell_type="adipocyte" 611575 /rano="pdapa7"	/org /db_		98401156 9731203	differences in gene expression of preed and age differences in gene expression 1/0 /3 713 710 /1000	Grindflek,E., Sundvold,H., Klungland,H. and Lien,S. Characterisation of porcine peroxisome proliferator activated	University of Norway, P.O. Box. 5025, 1432 As, NORWAY  ( bases 1 to 1640)	
Db .	o da vo	g da vy	Q	da	9 da 49	Db	Qy	Qy Db	Db	Db	Qy	Db	Дy	Db	Qy	Db 49	g b	Оу	Db	Qy	Db	Qy	ρ γ <sub>ζ</sub>	Db
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1497	CTAAGCTGCTCCAGAAATGACAGACCTCAGACAGATTGTGACAGAGCACGTGCAGCTG	w	ДЬ
418	AlaLysLeuLeuGlnLysMetThrAspLeuArgGlnIleValThrGluHisValGlnLeu	399	Qy
398 1437	uLeuGlnAlaLeuGluLeuGlnLeuLysLeuAsnHisProGluSerSerGlnLeuPhe 	379 1378	Qу Дъ
378 1377	euLeuAsnValLysProIleGluAspIleGlnAspAsn 	359 1318	Qy Db
w		Çî (	Db 23
i N	TAGAGAGCTAGAGAAAACCTTTATTTTTTTTTTTTTTTT		dd dd
338	ysSerLeuArgLysProPheGlyAspPheMetGluProLysPheGluPheAlaVal	-	Qy
<u> </u>	TIGATGAATAAAGACGGGGTCCTCATCTCCGAGGGCCAAGGATTCATGACAAGGAGTTT	w	Db 5
1137	aCCAAG!AAC!C!C!CAAAG!AIGGCG!CCACGAGAICATITACACCATGCTGGCCTCC enMetAssi.vsassGlvVali.e.iilleSerGliiGlvGlnGlvDheMetThrargGliiDhe	666 8/01	Q 5
298	AspGlnValThrLeuLeuLysTyrGlyValHisGluIleIleTyrThrMetLeuAlaSer	27	Qy
1077		1018	Db
	alGlnGluIleThrGluTvrAlaLysSerIleProGlyPheValAsnLeuAspLeuAsn	Ü	Οy
258 1017	GlnSerLysGluValAlaIleArgIlePheGlnGlyCysGlnPheArgSerValGluAla	239 958	Qy Db
957	TCCTTAATGATGGGAGAAGATAAAATCAAGTTCAAACACATCACCCCCCTGCAGGAG	9	DЬ
238	GluAspLysIleLysPheLysHisIleThrProLeuGlnGlu	219	Qy
9	GCGAGGCGATCTTGACAGGAAAGACCACAGACAAATCACCCTTTGTCATCTATGACATG	w	Db
218	aArgAlaIleLeuThrGlyLysThrThrAspLysSerProPheValIleTyrAspMet	199	. Qy
837	GCCCTGGCAAAGCACTTGTATGACTCATACATAAAGTCCTTCCCGCTGACCAAAGCAAAG	7	Db 47
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178	LeuLeuAlaGluIleSerSerAspIleAspGlnLeuAsnProGluSerAlaAspLeuArg [	159 718	γ γ
717	GGGATGTCTCATAACGCCATCAGGTTTGGGCGGATGCCACAGGCTGAGAAGGAGAAG	658	Db
158	ValGlyMetSerHisAsnAlaIleArgPheGlyArgMetProGlnAlaGluLysGluLys	139	Qy
657	ATCCACAAAAAAGTAGAAATAAATGTCAGTACTGTCGGTTTCAGAAATGCCTTGCT	598	фd
138	ArgAsnLysCysGlnTyrCysArgPheGlnLysCysLeuAla	125	Оу
597	TTCCGGAGGACTATCAGATTGAAGCTTATTTATGATAGGTGC		Дb
124		124	Qy
537	TGTGGGGATAAAGCCTCGGGGTTCCACTATGGAGTTCATGCTTGTGAAGGATGCAAG		Db
124		124	Qy
477		418	Db
124	lnLeuTyrAsn	121	Qy
417	GACTACCAAAGTGCCATCAAAGTGGAGCCTGTGTCCCCGCCTTATTATTCTGAAAAGACT	358	Db

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REFERENCE
AUTHORS
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

consecting by: Baylor College of Medicine Human Genomy
                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIAN at: http://image.llnl.gov Series: IRAK Plate: 24 ROW: 1 COlumn: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 675513
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence, Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Baylor Sequencing Center Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(bases 1 to 1782)
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                                                                                                                                                                                                                                    /clone="MGC:18439 IMAGE:4191539"
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1. .1782
EPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK
                                                                                                                    /db_xref="LocusID:19016"
                                                                                                                                /protein_id="AAH21798.1"
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                                                                                                                                                                             /product="peroxisome
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CAGCTCTACAACAGGCCTCATGAAGAACCTTCTAACTCCCTCATGGCCATTGAGTGCCGA 465
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                                                                                  GCGAGGGCGATCTTGACAGGAAAGACAACGGACAAATCACCATTTGTCATCTACGACATG
                                                                                                      AlaArgAlaIleLeuThrGlyLysThrThrAspLysSerProPheValIleTyrAspMet
                                                                                                                                                                                                                                                                                                                                      GTGGGGATGTCTCACAATGCCATCAGGTTTGGGCGGATGCCACAGGCCGAGAAGGAGAAG
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Mammalia; Eutheria; Rodentia; Sciurognathi
1 (bases 1 to 1780)
Tontonoz,P., Hu,E., Graves,R.A., Budavari,
MPPAR gamma 2: tissue-specific regulator of
Genes Dev. 8 (10), 1224-1234 (1994)
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Chordata;
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Vertebrata;
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US-09-931-007A-1 (1-688) x AB019561 (1-1518)
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Best Local Similarity:
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                                                                                                                                                                                                         LeuSerAlaAsnIleSerGlnGluMetThrMetValAspThrGluMetProPheTrpPro 40
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Direct Submission
Submitted (12-AUG-1998) Hiroshi Itoh, Kyoto University G.
School of Medicine, Dept of Med and Clin Sci; 54 Shogoin
Kawahara-Cho, Sakyo-ku, Kyoto 606-8507, Japan
(E-mail:hito@kuhp.kyoto-u.ac.jp, Tel:81-75-751-3170,
Fax:81-75-771-9452)
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Tanaka,T.
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/protein_id="BAA36485.1"
/db_xref="GI:4115709"
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/dev_stage="8-week-old"
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/strain="Sprague-Dawley"
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                       GCCAAGGTGCTCCAGAAGATGACAGACCTCAGGCAGATTGTCACAGAGCACGTGCAGCTA
                                  AlaLySLeuLeuGlnLySMetThrAspLeuArgGlnIleValThrGluHisValGlnLeu
                                                                                             LeuLeuGlnAlaLeuGluLeuGlnLeuLysLeuAsnHisProGluSerSerGlnLeuPhe
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Submitted (03-JUN-1999) Division
Institutet, C1-74 Huddinge Hospii
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Feltkamp,D., Gustafsson,J.A. and
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/db_xref="GI:5107415"
/translation="MGETLGDPPVDPEHGAFADALPMSTSQEITMVDTEMPFWPTNFG
/translation="MGETLGDPPVDPEHGAFADALPMSTSQEITMVDTEMPFWPTNFG
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GFFRRTIRKLIYDRCDLNCRHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEK
EKLLAEISSDIDOLNPESADLACHALKKHLYETPTTKASPPV
IYDMNSLMMGEDKIKFMHITPLQEQSKEVAIRIFGGCQFRSYEAVQEITTEYAKNIPFF
INLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEQGGFMTREFLKSLRKPFGDFM
EPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIODNLLQALELQLK
                                                                                                                                                                                                                                                                                                                                                                                                            LNHPESSQLFAKVLQKMTDLRQIVTEHVQLLHVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="peroxisome proliferator-activated 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawle
/db_xref="taxon:10116"
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tal, Huddinge S-141 86, Sweden
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                                          GACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGATCATCTACACCATGCTGGCCTCC
                                                                                                                                                                                                                                                                                                 CTGTTGGCGGAGATCTCCAGTGATATCGACCAGCTGAACCCAGAGTCTGCTGATCTGCGA
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      TyrLysAspLeuTyr
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                                                                                         LeuLysSerLeuArgLysProPheGlyAspPheMetGluProLysPheGluPheAlaVal
TACAAGGACTTGTAT
                                    LeuGlnValIleLysLysThrGluThrAspMetSerLeuHisProLeuLeuGlnGluIle 438
                                                            GCCAAGGTGCTCCAGAAGATGACAGACCTCAGGCAGATTGTCACAGAGCACGTGCAGCTA
                             CTGCATGTGATCAAGAAGACGGAGACAGATATGAGCCTTCACCCTCTGCTCCAGGAGATC
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Search completed: February 25, 2003, 05:32:08 Job time: 4897 secs

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Title:
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         SPTREMBL_21:*

SP_Archea:*

Sp_bacteria

Sp_bacteria

Sp_bacteria

Sp_fungi:*

Sp_invert

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16 1085.	15 1089.5	14 110	13 1117.	12 1141	11 1312.5	10 1325	9 1549	8 1564	7 1698	6 1916	5 1920	4 2045	3 2064	2 2089	1 2213	No. Score
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440	468	219	443	543	532	533	393	393	477	472	475	475	475	477	505	Length DB
1	σ	σ	13	13	13	13	13	<u>1</u> 3	13	13	13	11	σ	4	δ	DB.
Q99ND3	Q95N78	Q95KZ4	Q918W3	Q90WP6	Q9W712	Q9PW01	Q9PU26	Q9PU74	Q98SF8	Q8QGC0	Q91878	Q99PC7	Q95J17	Q96J12	Q95KZ8	ID
Q99nd3 rattus norv	Q95n78 canis famil	Q95kz4 mustela vis	Q9i8w3 gallus gall	Q90wp6 salmo salar	Q9w712 pleuronecte		Q9pu26 trachemys s		Q98sf8 xenopus lae	Q8qgc0 anser anser	Q9i878 gallus gall	Q99pc7 cavia porce	Q95j17 macaca fasc	Q96j12 homo sapien	Q95kz8 macaca fasc	Description

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1 MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF 60

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392.5	394.5	509.5	571.5	684.5	715	738	802.5	935	969	1000	1020.5	1021.5	1028.5	1033	1035.5	1056	1065.5	1067.5	1068.5	1070	1070.5	1076.5	1076.5	1076.5	1078.5	1080.5	1082	1084.5
11.2	11.2	14.5	16.3	19.5	20.4	21.0	22.9	26.7	27.6	28.5	29.1	29.1	29.3	29.4	29.5	30.1	30.4	30.4	30.5	30.5	30.5	30.7	30.7	30.7	30.7	30.8	30.8	30.9
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Q922a5 mus musculu	Q90970 gallus gall	075780 homo sapien	046477 oryctolagus	Q8uux2 pimephales	Q9w718 gallus gall	Q9glg8 mustela vis	Q9bud4 homo sapien	Q90y02 petromyzon	Q9i8f7 salmo salar	046479 oryctolagus	Q9pu75 crocodylus	Q90z62 salmo salar	Q9n135 sus scrofa	070527 cavia porce	Q90z67 brachydanio	CL.	Q9n129 bos taurus	Q9n128 bos taurus	Q9i8w4 gallus gall	Q8qgcl anser anser	Q8uux1 oryzias lat	Q9n2h4 oryctolagus		Q90z66 brachydanio	Q9i8f6 salmo salar	-	Q8wms4 canis famil	Q9mzg4 sus scrofa

## ALIGNMENTS

RESULT 1  10 958X28

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Best I
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Q96J12;
01-DEC-2001
                                                                                                                                                                                                                                                                InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
ProDom; PD000035; Znf_C4steroid; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
                                                                                                                                                                                              Zinc-finger
SEQUENCE
                                                                                                                                                                                                                                           DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY) .
i- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR EMBL; BC006811; AAH06811.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
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                  MTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDP 88
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                                                                                                                        Similarity
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                                                                                              Mismatches
                                                                                   e 2089; pb ...
1. No. 3.2e-123;
1. hes 0;
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                                                                                                Matches
                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                   Zhou J., Wilson K.M., Medh J.D.;
Zidentification of novel peroxisome proliferator-activated gamma splice variants and induction of PPAR-gamma expressioning the particle of the submitted diet in monkey macrophages.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SUBCELLULAR INCATION: NUCLEAR HORMONE RECEPTORS FAEMBL; AY048696; AAL05231.;
-- EMBL; AY048696; AAL05231.;
-- EMBL; AY048694; AAL05231.;
-- EMBL; AY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95J17 PRELIMINARY; PRT; 475 AA.
Q95J17;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Peroxisome proliferator-activated receptor gamma 3
proliferator-activated receptor gamma 1).
                                                                                                                                                                                                                                                                Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
ProDom; PD000035; Znf_C4steroid; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumanmalia; Eutheria; Primates; Catarrhini; Cercopithecice; Macaca.
                                                                                                                                                                                                                                         DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9541;
[1]
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                                                                                                                                                                                                                  Zinc-finger
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MVDTEMPFWPTNFGISSVDLSVMDDHSHSFDIKPFTTVDFSSISAPHYEDIPFTRTDPMV
                                                                                              al Similarity
409; Conserv
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                                                                                              58.8%; ilarity 86.1%; Conservative
                                                                                                                                                                                              AA;
                                                                                                                                                                                              54470 MW;
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                                                                                      Score 2064; DI
Pred. No. 1.2e
2; Mismatches
                                                                                              2
                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                              D16C3A931EB89181 CRC64;
                                                                                                                                                                                                                                         Transcription regulation
                                                                                              DB 6;
.2e-121;
les 2;
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                                                                                                                                         Length
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       Matches
                                 Best
                                                   Query Match
                                                                                                                                                                                                                                                                  InterPro; IPRO00536; Hormone_rec_lig.
InterPro; IPRO01723; Stdhrmn_receptor.
InterPro; IPRO01628; Srd_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STROIDEINGER.
PRINTS; PR00047; STROIDEINGER.
PRODOm; PD000035; Znf_C4steroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99PC7 PRELIMINARY; PRT; 475 AA.
Q99PC7;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-CCT-2001 (TrEMBLrel. 18, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Peroxisome proliferator activated receptor-gamma (Fragment).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-ADIPOSE TISSUE;
Khoo B.Y., Najimudin N., Tengku Muhammad T.S.;
Khoo B.Y., Najimudin N., Tengku Muhammad T.S.;
"Molecular Cloning and Sequencing of Peroxisome Prolifer
Receptor-gamma (PPARgamma) from Guinea Pig.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
EMBL; AF317514; AAG60685.2; -.
                                                                                                                                                                                                                              SMART;
SMART;
                                                                                                                                                      Zinc-finger.
                                                                                                                                                                               DNA-binding; Nuclear
                                                                                                                                                                                                         PROSITE; PS00031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS
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       404;
                                                                                                                                                                                                                              SM00430; HOLI; 1.
SM00399; ZnF_C4; 1.
                               Similarity
                                                                                                       475
       Conservative
                                                                                                                                 <u>ب</u>
                                                                                                       AA;
                                                                                                                                                                                                       NUCLEAR_RECEPTOR;
                                                                                                    1
54425
                                                                                                                                                                             protein;
                                 85
85
                               . 18;
                                                      .3°
                                                                                                       MW;
Score 2045; DB 11;
Pred. No. 1.9e-120;
""cmatches 4;
                                                                                                                                                                             Receptor;
                                                                                                    DE45CF49C896F401 CRC64;
                                                                                                                                                                          Transcription
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                                              Length
     Indels
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                                                                                                                                                                             regulation
                                                   475;
  62;
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  Gaps
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Meng H., Li J., Zhao J., Wang Q., Li H.;
"The SNPS detection on exon 2 of PPAR gamma gene
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ dat
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RE
EMBL; AB045597; BAA98100.1; -.
EMBL; AB045597; AA981070.1; -.
                                                                                                                              activated receptor-alpha phenotype.";
                                                                                                                                                                       MEDLINE=20267232; PubMed=10809235; Takada I., Yu R.T., Xu H.E., Lambe Evans R.M., Umesono K.;
                                                                                                                                                                                                                                  "Characterization of a cDNA sequence encoding the peroxisome proliferator activated receptor gamma in broiler chicken."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           Archosauria; Aves; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91878;
01-OCT-2000
                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20267232; Pi Takada I., Yu R.T.,
                                                                                                                                                                                                                                                                                                                                                              Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91878
                                                                                     TISSUE=BLOOD;
                                                                                                                                                                                                                                                                          Sato K., Akiba Y.;
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                          PPAR GAMMA
                                                                                                                                                                                                                                                                                                                                                                                     proliferator-activated receptor
                                                                                                   SEQUENCE FROM
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                                                                                                                          Endocrinol.
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                                                                                                                                                                                                                                                                                                                                     Neognathae;
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Neognathae; Galliformes; Phasianidae;
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a (PPAR
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                                                                                                                                                R alpha)
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                        RECEPTORS FAMILY
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a PPAR delta
                                                             'n
                                                                                                                                                                                    V.G.,
                                                             chicken
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Pfam; PF00105; zf-C4; 1.

Pfam; PF00105; zf-C4; 1.

PRINTS; PR000398; STRDHORMONER.

PRINTS; PR00037; STROIDFINGER.

PRODOM; PD000035; Znf_C4steroid; 1.

SMART; SM00439; HOLI; 1.

SMART; SM00399; ZnF_C4; 1.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

DNA-binding; Nuclear protein; Receptor; 1.

Zinc-finger.

Zinc-finger.
              Meng H., L
Submitted
                                                                                                                            Q8QGC0 PRELIMINARY; PRT; 472 AA.
Q8QGC0;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Peroxisome proliferator-activated receptor gamma (Fragment).
                                   TISSUE=FAT;
                                                                                    Archosauria;
                                                                                               Eukaryota; Metazoa;
                                                                                                            Anser anser (domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
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HSSP; P37231;
                                                 SEQUENCE FROM N.A.
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 tted (FEB-2002) to the AF481798; AAL87700.1;
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                         Li H.;
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                                                                                    Aves; Neognathae;
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                                                                                             ic goose).
Chordata; Craniata; Vertebrata;
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80.0%;
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            EMBL/GenBank/DDBJ
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Pred. No. 1
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                                                                                    Anseriformes; Anatidae;
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ches 19;
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                                                                                               Euteleostomi;
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Matches
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                                                                                                 "Structural and functional analysis of PPARs.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS EMBL; AJ310087; CAC34402.1; -.
HSSP; P37231; 1FM9.
                                                                                                                                                                                                                                                                                                                   Q98SF8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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           PRINTS;
                                                           InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                               Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Amphibia; Batrachia;
                                     Pfam; PF00104; hormone_rec; Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                               Escher P.;
                                                                                                                                                                                          TISSUE=FAT BODY;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                           Peroxisome proliferator-activated
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378; Conser
PR00398; STRDHORMONER.
PR00047; STROIDFINGER.
PD0000035; Znf_C4steroid;
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472 i
                                                                                                                                                                                                                                                       Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                           Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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54095 MW;
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                                                              Stdhrmn_receptor.
Znf_C4steroid.
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD17ED2FB8FAFD25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                           receptor gamma
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                                                                                                                             RECEPTORS
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                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                        472
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Best L
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                                                                                                                                                                                                                                                                     Q9PU74;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                   Crocodylus niloticus (Nile crocodile) (African crocodile)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
                                                                                                                                                                                                                                              PPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor
Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
 Pfam;
Pfam;
                                                          "Warm-blooded isochore structure in nile crocodile Mol. Biol. Evol. 16:1521-1527(1999).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECE EMBL, AJ243132; CAB61238.1; -.

HSSP; P37231; 1FM9.
                                                                                                                                                                                                                                                                                                                     Q9PU74
                     InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                             MEDLINE=20022983; PubMed=10555283;
                                                                                                                                                                                             NCBI_TaxID=8501;
                                                                                                                                                                                                           Archosauria;
                                                                                                                                                                                                                                                         Peroxisome
                                                                                                                                                                                                                                                                                                                                                                                 418
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                                                                                                                                                                                                                                                                                                                                                                                                                              KPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGRATDKTPVVIHDMNSLMMGEDQIKGQCVSP--EQNKEVAIRIFQRCQSRSAEAVREIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEIT
                                                                                                                                                                                                                                                                                                                                                                             ELQLKLNHPDSAQLFAKLLQKMTDLRQVVTEHVQLLQLIKKTEADMCLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASGFHYGVHACEGCKGFFRRTIRLKLIYERCDLNCRIHKKSRNKCQFCRFQKCLAVGMSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------NRNKCQYCRFQKCLAVGMSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYDTEMPFWSNLNFGMNSMDMSALEDHCQPYDIKPFTTVDFSSINS-HYDDILDEKTFLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFAKNIPGFVSLDLNDQVTLLKYGVHEIIFTMLASLMNKDGVLVAEGQGFMTREFLKSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAIRFGRMPQAEKEKLLAEISSDIDQLNPESADQRVLAKHLYDSYVKSFPLTKAKARAIL
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            PF00104; hormone_rec;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00430; HOLI; 1.
SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                        ) (TYEMBLIEL 13, Created)
(TYEMBLIEL 13, Last sequence update)
(TYEMBLEL 11, Last annotation update)
proliferator activated receptor gamma
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                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                          Crocodylidae;
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70.8%;
                                                                                                                                                                                                          Crocodylinae;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                         Crocodylus
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                                                                                                                                                                                                                                                         gamma (Fragment).
                                                                                                                                                                                                                                                                      update)
                                                                                  RECEPTORS
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                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                      turtle
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                                                                                  FAMILY
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
        -!- SUBCELLULAR LOCATION: NUCLEAR (F-!- SIMILARITY: BELONGS TO THE NUCLE BHBL; AJ24313; CAB61263.1; -- HSSP; P37231; 1FM9.
InterPro; IPR000536; Hormone_rec_lig InterPro; IPR001723; Stdhrmn_recepto_InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                 Q9PU26;
Q9PU26;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
                                                                                    Hughes S., Zelus D., Mouchiroud D.; "Warm-blooded isochore structure in Mol. Biol. Evol. 16:1521-1527(1999).
                                                                                                          MEDLINE=20022983; PubMed=10555283; Hughes S., Zelus D., Mouchiroud D.
                                                                                                                                                                Testudines; Cryptodira; NCBI_TaxID=31138;
                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                      Trachemys scripta elegans.
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                              PPAR
                                                                                                                                                                                                                         Peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00398; STRDHORMONER. PRINTS; PR00047; STROIDFINGER. ProDom; PD000035; Znf_C4steroid;
                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
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Local 5.
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                                                                                                                                                                                                                                                                                                                                                 QKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVT
                                                                                                                                                                                                                                                                                                                                    QKMTDLRQIVTEHVQLLQIIKKTETDMSLHPLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTIRLKLIYDRCDLNCRIHKKGRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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393
393 AA;
                                                                                                                                                                                                                        proliferator
                                                                                                                                                                                                                                  (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
393
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         Hormone_rec_lig.
Stdhrmn_receptor
Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.68;
79.98;
                                                                                                                                                                                                                  13, Created)
13, Last sequence update)
21, Last annotation update)
activated receptor gamma (Fragment).
                                                                                                                                                                            Testudinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1564;
Pred. No. 2
                                                                                                                                                                                      Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                               NUCLEAR
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                                                                                                                                                                            Emydidae;
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                                                               HORMONE
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                                                                                                                                                                                      Vertebrata;
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                                                                                                                                                                                                                                                                              ΑA
                                                                                                crocodile
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                                                                 RECEPTORS
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                                                                                                                                                                             Trachemys
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                                                                                                 and
                                                                                                                                                                                      Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation;
                                                                 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 10
Q9PW01
ID Q9PW0
AC Q9PW0
AC Q9PW0
DT 01-MA
DT 01-JU
DE PPARC.
GN PPARC.
OS Pleur
OC Eukar
OC Acant
OC Acant
OC ACACT
OC ACACT
COT
ISSU
RN [1]
RP SEQUE
RA Leave
RT Marin
RL Leave
RT Marin
RL Submi
CC -!- S
CC -!- S
CC -!- S
CC II-SU
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Best Loc
Matches
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PRINTS; PR00398; STRDHORMONER.

PRINTS; PR00047; STROIDFINGER.

ProDom; PD000035; Znf_C4steroid; 1.

SMART; SM00430; HOLI; 1.

SMART; SM00399; ZnF_C4; 1.

SMART; SM00399; ZnF_C4; 1.

PROSITE; PS00031; NUCLEAR RECEPTOR; 1

DNA-binding; Nuclear protein; Receptor
Zinc-finger.
    JUDMITTEE (AUG-1956) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOPS EMBL; AJ243956; CAB51618.1; -.
HSSP: P37231; 1FM9.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                  Q9PW01 PRELIMINARY; PRT; 533 AA.
Q9PW01;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                   Pleuronectes platessa (Plaice).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Pleuronectidae; Pleuronectes.
                                                                                                               SEQUENCE FROM N.A. TISSUE=GILL;
Leaver M.J.;
                                                                                                                                                             NCBI_TaxID=8262;
[1]
                                                                                                                                                                                                                                                         Peroxisome proliferator-activated receptor gamma \ensuremath{\mathsf{PPAR}} .
                                                                                                                                                                                                                                                                                                                                                                                                                                           403
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Local Sim
hes 313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMFQAEKEKLLAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LELDDSDLAIFIAVIILSGDRPGLLNVKFIEDIQDNLLQALELQLKLNHPESSQLFAKLL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGEDQINCKHVTPLQEQNKEVAIRIFQRCQFRSVEAVQEITEFAKSIPGFVNPDLNDQVT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLKYGVHEIIYTLLASLMNKDGVLISNGQGFMTREFLKSLRKPFCDFMEPKFEFAVKFNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LELDDSDLAIIIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLL
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393
393 AA;
  IPR000536;
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393
; 44812 MW;
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79.6%;
Hormone_rec_lig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.8e-89
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                                            RECEPTORS FAMILY
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	Craniata; Vertebrata; Euteleostomi; Cleostei; Euteleostei; Neoteleostei; ; Percomorpha; Pleuronectiformes; e; Pleuronectes.	Pleuronectes platessa (Plaice) Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; T Acanthomorpha; Acanthopterygi	888888
	ted) t sequence update) t annotation update) ed receptor gamma.	01-NOV-1999 (TrEMBLrel. 12, Cres 01-NOV-1999 (TrEMBLrel. 12, Las 01-JUN-2002 (TrEMBLrel. 21, Las Peroxisome proliferator-activat	
	T; 532 AA.	ULT 11 1712 Q9W712 PRELIMINARY; PRT	RES Q9W
		529 MKDLY 533	Db
		439 YKDLY 443	Qy
	Ñ	69	Db
	TDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEI 438	379 LLQALELQLKLNHPESSQLFAKLLQKMI	Qy
	FORMERKEEFAVKNALELDDSDLAIFLAVIILSGDRPGLLNVKPIEDIQUN 3/8	319 LKSTRKPEGDEMERKEEFAVKENALELLE	Дy
	YGQIFMTREF 40	49 VREVTEF	Дb
	EGQGFMTREF 31	G	Qy
	DYGVWGTTSISGQEPQNALELRFFQSCQSRSAEA 348	HMGS	DЪ
	EVAIRIFQGCQFRS	234 TPLOEOSK	Qy
	Q 28	9 4	Db dd
	KHI 23	74 SADLE	0 0
	KTQLYNRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPE 173	7	P 99
	RVCGDKASGFHYGVHACEGCKGFFRRTIRLKLVYDH 168	109 QYSDSPVFSKLQDDTTAASLNIECRVCG	ДЪ
	118	115 YYSE	Qy
	:     ::  :	61 ISSVGMAYDDSPPQSEEHLTNWDYTNMHSYRTEPNV-	DЬ
	DYKYDLKLQEYQSAIKVEPASP	76	Qy
	SHSLDMKHLATLDYTSISSASVPSSLSPQLMSS 60	1 MVDTQQLLFWPVGFSLSAVDLSELDDSS	ДD
	HSFDIKPFTTVDFSS	GISSVDLSVMED	Qy
6	1325; DB 13; Length 533; No. 3e-75; smatches 66; Indels 144; Gaps	uery Match est Local Similarity 50.6%; Pred. atches 276; Conservative 59; Mi	Qu Be Ma
	D3955E777961300 CRC64;	SEQUENCE 533 AA; 60513 MW; DD3	
	<pre>DR; 1. ceptor; Transcription regulation;</pre>	PROSITE; PS00031; NUCLEAR_RECEPTOR DNA-binding; Nuclear protein; Rece	DR
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	_	PRINTS; PRO0398; STRDHORMONER. PRINTS; PRO0047; STROIDFINGER. PRODOM: DD000035: Znf C4steroid:	
	eptor.	roi	

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Best Local Similarity
Matches 275; Conserv
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-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

EMBL; AJ249075; CAB51396.1; JOINED.

EMBL; AJ249076; CAB51396.1; JOINED.

EMBL; AJ249077; CAB51396.1; JOINED.

EMBL; AJ249078; CAB51396.1; JOINED.

EMBL; AJ249078; CAB51396.1; JOINED.

EMBL; AJ249078; CAB51396.1; JOINED.

EMBL; AJ249080; CAB51396.1; JOINED.

EMBL; AJ249080; CAB51396.1; JOINED.

EMBL; AJ249080; CAB51396.1; JOINED.
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ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM0039; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-Dinding; Nuclear protein; Receptor; Transcription regulation;
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Leaver M.J.;
"A peroxisome proliferator-activated receptor gamma gene fish.";
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00104; hormone_rec; Pfam; PF00105; zf-C4; 1.
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InterPro; IPR001628; Znf_C4steroid.
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528
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                                           YKDLY 443
                                                                                                                                                                                                                                                                                                                                                                                                                                        TPLQEQSK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDLHCRIHKKSRNKCQYCRFQKCLNVGMSHNAIRFGRMPQAEKEKLLAEFSSDMEHMHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYSDSPVFSKLQDDPTAASLNIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLVYDH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YYSE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISPVGMAYDPSPPQSEEHLTNMDYTNMHSYRTEPNV------HNSIKMEPESPP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVDTQQLLAWPVGFSLSAVDLSELDDSSHSLDMKHLATLDYTSISSASVPSSLSPQLMSS
                                                                                                                                                                                                                                                                                                                                                                                   -PIQEQQQASVLTAAHGGLTEVHMGSDYGVWGMTSISGQEPQNALELRFFQSCQSPSAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PHYEDIPFT-----RTDPVVADYKYDLKLQEYQSAIKVEPASPP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 AA; 60176 MW; A3E216B79BDC7E9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.4%; Score 1312.5; DB 13; Length 532; 50.5%; Pred. No. 1.8e-74; tive 60; Mismatches 65; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EVAIRIFQGCQFRSVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from a
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	12
ID 090	WP6 PRELIMINARY; PRT; 543 AA.
DT 01-	EMBLrel. 19, Created)
DT 01-	JUN-2002 (Trembirel. 19, Last sequence update)
GN PPA	oxisomal proliferator-activated receptor gamma. R GAMMA.
OS Sal	to look
OC Act	aryota; Metazoa; Cnordata; Craniata; Vertebrata; Euteleostomi; inopterygii; Neopterygii; Teleostei; Euteleostei;
OC Pro	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo. NCBI_TaxID=8030;
RN [1]	HENCE FROM N A
RA Fon	
RT "IS	מכים
-i-	SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
. i -	SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMB	E; AJ416951; CAC95230.1;
DR Int	erPro; IPR001628; Znf_C4steroid.
סלם pfa	m; PFUULU4; normone_rec; 1.
DR Pro	Dom; PD000035; Znf_C4steroid; 1.
KW DNA	-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zin SQ SEQ	
Query Best L	Score 1140; DB 13; Length 54 Pred. No. 1.2e-63;
	מן כטווסבדיאנידיה טטן איבאוומרנונס דטטן דוומבדס דטיי, ממף
Qy 3	1 MVDTEMPFWP-TNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIP 82
Db	
Оу 8	3FTRTDPVVADYK
Db 6	1 DRSHSCNHSPDRSHSFNHSPDRSHSFNHSPDRNHSFNHSPDRSHSFNHSPDRSHSYND 118
Оу 9	8 KLQEYQSAIKVEPAS 124
Db 11	9 TYSVYQGSVNDKPLSPSQSSDCSIVSLSRPRPHSNPPTYTDASSLLNIDCRVCGDKASGF 178
Qy 12	5
Db 17	9 HYGVHVCEGCKGFFRRTVRLKLVYDHCDLHCRIHKKSRNKCQYCRFQKCLLVGMSHDAIR 238
Qy 14	- R
Db 23	9 FGRMPQVEREKLLQAEFMDVEPRNPESADLRALSRQLCLSYHRHFPLTKSKAKAILSGKT 298
Оу 208	TDKSPFVIYDMNSLMMGEDKI
Db 299	
Qy 25	9 VQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREF 318
Db 35	9 VQEVTEFTKSIPGFTELDMNDQVILLKYGVIEVMTTMLAPLMNKDGTLFAYGQIFMTREF 418
Оу 319	LKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVI
Db 419	9 LKSLRKPFCEMMEPKFEFAAKFNLLELDDSDMALFFAVIILSGDRPGLVNVKPIEDLQET 478
Оу 37	9 LLQALELQLKINHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEI 438
Db 47	)CPQLFAKLLQKMTDLRQLVANHVRHIHLLKKQ

Qy

439

YKDLY

443

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Qy
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                                                                                                                Qy
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Best Local
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR00053; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PFINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PRODOm; PD000035; Znf_C4steroid; 1.
SMART; SM00399; Znf_C4; 1.
SMART; SM00399; Znf_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O918W3
Q918W3;
01-OCT-2000 (TrEMBLrel, 1:
01-OCT-2000 (TrEMBLrel, 1:
01-JUN-2002 (TrEMBLrel, 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Endocrinol. 14:733-740(2000).

-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)

-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE REEMBL; AF163810; AAF80480.1; --
HSSP; P03372; 1HCQ.
                                                                                                                                                                                                                                                                                                                                                      DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
SEQUENCE 443 AA; 50108 MW; EB6E0C39554C76CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenotype."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takada I., Yu R.T., Xu H.E., Lambert M.H.,
Evans R.M., Umesono K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20267232; PubMed=10809235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Archosauria; Aves; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alteration of a single amino acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                        242
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              302
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             KDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSG
                                    SDSFTD---TLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRDLY
                                                                                                                                           NRNKCQYCRFQKCLSLGMSHNAIRFGRMPEAEKRKLVAGLTASEISCQNPQVADLKAFSK
                                                                                                                                                                                                                                                SSSYTDLSQSSSPSLSDQLQMGCEE----TASGALNVECRVCGDKASGF------
                                                                                         HIYNAYLKNENMTKKKARGILTGKASSTPQPFVIHDMDTLWQAEKGLVWKQLVNGIPPYK
                                                                                                                 HLYDSYIKSFPLTKAKARAILTGK-TTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSK
                                                                                                                                                                                                                       SSISTPHY-----EDIP--FTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLY 123
                                                                                                                                                                                                -----HYGVHACEGCKGFFRRT-----IRMKL-EYEKCER-----
Similarity
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                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Eute
Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                31.9%;
53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15, Created)15, Last sequence update)21, Last annotation updat
                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                   Score 1117.5;
Pred. No. 2.4e:
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                     EB6E0C39554C76CD CRC64;
443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   generates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peroxisome
                                                                                                                                                                                                                                                                                                                 .4e-
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                                                                                                                                                                                                                                                                                                    88; Indels
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a PPAR delta
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                                                                                                                                                                                              SCKIQKK 121
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                                                                                                                                                                                                                                                                                                                            443;
                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 15
Q95N78
Q95N7
ID Q95N7
AC Q95N7
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-JU
DE Perox
OS Canis
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Q95KZ4
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Best Local Similarity
Matches 218; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
EMBL; AV050524: AALI1452.1; -.
InterPro: IPPNONGS --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       095KZ4 PRELIMINARY; PRT; 219 AA. 095KZ4; 095KZ4; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Peroxisome proliferator-activated receptor gamma (F)
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR01628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Desmarais J.A., Bennett R.

"Mustela vison Peroxisome
mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mustela vison (American mink).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; Nuclear protein; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mustela.
                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9667;
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                                                                                                                                                                    CLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLT
                                                                                                                          REFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFI 219
                                                                                                                                               REFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDGLLVANGNGFVTREFLRTLRKPFNEIMEPKFEFAVKFNALELDDSDLSLFVAAIILCG
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219
219
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                     AA;
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Peroxisome Proliferator-Activated
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219
24828 Þ
                                                                                                                                                                                                                                                                                                                  31.5%;
                                                                                                                                                                                                                                                                                                                                                     MW.
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                                                                                                                                                                                                                                                                                                        Score 1105; E
Pred. No. 5.7e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                  5.7e-62;
                                                                                                                                                                                                                                                                                                                                                                                               Transcription
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                                                                                                                                                                                                                                                                                                                             6; Length
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O95N78
O95N78
O95N78;
O95N78;
O1-DEC-2001 (TrEMBLrel. 19, Createu,
O1-DEC-2001 (TrEMBLrel. 19, Last sequ
OT 01-JUN-2002 (TrEMBLrel. 21, Last ann
Deroxisome proliferator activated re

Created)
Last sequence up

update) update)

468

AA

receptor alpha

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A NAGASAWA M., Ide T., Murakami K.;

A NAGASAWA M., Ide T., Murakami K.;

Yi Nog PPAR alpha cDNA sequence.";

Yi Dog PPAR alpha cDNA sequence.";

Yi Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

'-- SIMILARITY: BELONGS TO THE NUCLEAR (BY SIMILARITY).

'-- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

YI EMBL; AF350327; AAX38655.1; --

YI INTERPO; IPR000536; Hormone_rec_lig.

InterPro; IPR001688; Znf_C4*Steroid.

Pfam; PF00104; hormone_rec; 1.

YI Pfam; PF00105; Znf_C4* 1.

PR Pfam; PF00105; Znf_C4* 1.

PROSITE; P$000031; NUCLEAR_RECEPTOR; UNKNOWN_1.

PROSITE; P$000031; NUCLEAR_RECEPTOR; UNKNOWN_1.

NO SECUENCE Af6 No. 52122 Mg. 1122C2EARETERE COCCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; (
Mammalia; Eutheria; (
NCBI_TaxID=9615;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              137
461
                                                             401
                                                                                                                             341
                                                                                                                                                                                                                                                                                                                              162
                                                                                                                                                            316
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                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                        222 KVKARVILAGKASNNPPFVIHDMETLCMAEKTLVAK-LVANGIQNKEAEVRIFHCCQCTS
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                                                                                                                                                                                                                                                                                                                                                                                           106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 --FTEYQYLGSGPGSDGSVITDTLSPAPSPSSVTHP---AAPGGAEEPSSVALNIECRIC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 DSPIDP----ESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ū
                                                                                                                          REFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFTAVIILSGDRPGLLNVKPIEDI 375
                                                                                                                                                                                                             VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMT 315
                                                                                                                                                                                                                                                                              KAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRS
             QEIYKDLY 443
                                                                              QDNLLQALELQLKLNHPESSOLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLL 435
                                                                                                                                                                                                                                                                                                                        LAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHLYDSYIKSFPLT 195
                                                                                                                                                                                                                                                                                                                                                                                           GDRASGYHYGVHACEGCKGFFRRTIRLKLA----YDKCDRSCKIQKKNRNKCQYCRFHKC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPFTTVDF---------SSISTPHYEDIPFTRTDPV------
QEIYRDMY 468
                                                             QEGIVHVLKLHLQTNHPDNIFLFPKLLQKMADLRQLVTEHAQLVQVIKKTESDAALHPLL
                                                                                                                                                                                           VETVTELTEFAKSIPGFANLDLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNGFIT 340
                                                                                                                                                                                                                                                                                                                                                                                                                         ---VADYKYDLKLQE-----YQSAIKVEPASPPYYSE-----KTQLYNRNKCQYCRFQKC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPICPLSPLEADDLESPLSEEFLQEMG------NIQEISQSIGEDSSGSFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 AA; 52122 MW; 11F2C2F9AAB176D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1089.5; DB 6; Length 468; Pred. No. 1.5e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                           460
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Search completed: February 25, 2003, 04:00:31 Job time: 79 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
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Match
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RORA_HUMAN
RORA_MOUSE
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               rattus norv
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homo sapien
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## ALIGNMENTS

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Gene Expr. 4:281-299(1995).  [5]  SEQUENCE FROM N.A. (ISOFORM 1).  TISSUE=Placenta; MEDLINE=98016122; PubMed=9356045; Okazawa H., Mori H., Tamori Y., Araki S., Niki T., Masugi J., Okazawa H., Mori H., Tamori Y., Araki S., Niki T., Masugi J., Rawanishi M., Kubota T., Shinoda H., Kasuga M.; "No coding mutations are detected in the peroxisome proliferator- activated receptor-gamma gene in Japanese patients with lipoatrophic diabetes."; Diabetes 46:1904-1906(1997).	and characterization of huma ted receptors gamma 1 and gam BL/GenBank/DDBJ databases.  BL/GenBank/DDBJ databases.  BL/GenBank/DDBJ databases.  BL/GenBank/DDBJ atabases.  BL/GenBank/DDBJ atabases.  BL/GenBank/DDBJ atabases.  Composition of huma topoietic cells and chromosom	SEQUENCE FROM N.A. ( SEQUENCE FROM N.A. ( TISSUE-Heart; MEDLINE-97218249; Pu Mukherjee R. Jow L. "Identification, cha peroxisome prolifera peroxisome prolifera versus ppargammal an antagonists."; J. Biol. Chem. 272:8 [2] [2] [2] SEQUENCE FROM N.A. ( TISSUE-Fat body; Elbrecht A., Chen Y.	SUL AT_

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NR1 SUBFAMILY

DISEASE: DEFECTS IN PPARG COULD PLAY A ROLE PREDISPOSITION TO OBESITY.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE I

NUCLEAR HORMONE RECEPTOR FAMILY

IN THE GENETIC

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Sarraf P., Muc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 severe insulin resistance, diabetes mellitus and hypertension.";
Nature 402:880-883(1999).
-i- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamann A., Munzberg H., Buttron P., Busing B., Hinney A., Mayer H. Siegfried W., Hebebrand J., Greten H.; "Missense variants in the human peroxisome proliferator activated receptor gamma2 gene in lean and obese subjects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yen C.-J., Beamer B.A., Negri C., Silver K., Brown K.A., Yarna Burns D.K., Roth J., Shuldiner A.R.;
"Molecular scanning of the human peroxisome proliferator active receptor gamma (hppAR-gamma) gene in diabetic Caucasians: identification of a prollala PPAR-gamma-2 missense mutation.";
Biochem. Biophys. Res. Commun. 241:270-274(1997).
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"Asymmetry in the PPARgamma/RXRalpha crystal structure reveals the molecular basis of heterodimerization among mucles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [6]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chatterjee V.K.K., O'Rahilly S.; "Dominant negative mutations in human PPAR-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barroso I., Gurnell M., Crowley V.E.F., Agostini M., Soos M.A., Masien G.L., Williams T.D.M., Lewis H., S
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MEDLINE=99337654; PubMed=10407229;
MEDLINE=99337654; PubMed=10407229;
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New Engl. J. Med. 339:953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS DIABETES MET-318 AND LEU-495. MEDLINE=20085964; PubMed=10622252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS COLON CANCER PRO-314 AND MEDLINE=99322672; PubMed=10394368;
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activated by inducers of adipogenesis, including thiazolidinedione
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambe K.G., Tugwood J
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PLACENTA,
DISEASE: I
DIABETES !
                                                                                                                                             HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS TH
PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR
OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.
SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
SUBCELLULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 AND 2 (SHOWN HERE);
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE. LOWER IN
                                                                                                                     SKELETAL MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mueller E., Smith W.M., Wright H.N.A., de la Chapelle A., Spiegelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 3:799-804(1999).
                                            DEFECTS
                                                                                LUNG AND OVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239:1-7(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutations in PPAR-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339:953-959(1998).
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                                            IN PPARG
                                                                                                                     SPLEEN,
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                                                                                                                     HEART
                                        CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfeiffer
                                        LEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIS-316,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wright H.M.,
                                                                                                                 AND LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic
                                        TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           man B.M., Eng
associated w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferator activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В.М.,
                                                                                                                     ALSO
                                        N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with hypertension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W., Kahn C.R.; regulator of
                                        INSULIN-RESISTANT
                                                                                                                     ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schafer A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IJ.B.,
Eng C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schwabel J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with human colon
                                                                                                                 DETECTABLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALA-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mayer H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        THE
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HYPTERTENSION

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CONFLICT
CONFLICT
SEQUENCE
                                       CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1FM6;
PDB; 1FM9;
TRANSFAC; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
PIR; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                  Obesity;
                                                                                                                                                                                                                                                                                                                                   SMART; SM00430; HOLI; 1
SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       VARIANT
                                                                                           VARIANT
                                                                                                                           VARIANT
                                                                                                                                                          VARIANT
                                                                                                                                                                             VARIANT
                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                       Receptor; Transc:
Nuclear protein;
                                                                                                                                                                                                                                                                                                               PROSITE; PS00031; NUCLEAR_RECEPTOR; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:9236; PPARG MIM; 601487; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00105;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                    ZN_FING
                                                                                                                                                                                                                                                                                             Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; AB005526; BAA23354.1; ALT_INIT.

(AB005521; BAA23354.1; JOINED.

(AB005523; BAA23354.1; JOINED.

(AB005523; BAA23354.1; JOINED.

(AB005524; BAA23354.1; JOINED.

(AB005525; CAA62152.1; ALT_INIT.

(AS00563; CAA62153.1; -1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             604367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S42489; S42489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U79012; AAC51248.1;
U63415; AAB04028.1;
D83233; BAA18949.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L40904; AAA80314
                                                                                                                                                                                                                               3D-structure
139 203
139 159
176 198
318 505
112 112
                                                                                                                                                                                                                                                                                                                                                                                                            IPR000536;
IPR001723;
IPR001628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 16-FEB-01
T03731; -.
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        505
                 36
213
240
424
                                                                       495
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                                                                                                                           316
                                                                                                                                                          314
                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                        zf-C4;
                                                                                                                                                                                                                                                                                                                                                                                                   hormone_rec;
37
214
240
426
57620 .
                                                                                                                                                                                                                                                                                            Polymorphism;
                                                                                                                                                                                                                                                                                                       Zinc-finger; Multigene family; Alternative
                                                                     495
                                                                                                                                                                            113
                                                                                                                                                                                                 30
12
                                                                                                                                                                                                                                                                                                                                                                                                            Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                        Stdhrmn_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hormone_rec_lig
        MΣ,
                                                                                                                                                      /FTId=VAR_010724
Q -> P /TW -
      R -> RQ (IN REF. 3 AND 4).
MISSING (IN REF. 5).
3933EFF36A0E4CAF CRC64;
                             MP ->
                                                                     V -> M (IN DIABETES).
/FTId=VAR_010727.
P -> L (IN DIABETES).
                                                                                                                                                                           /FTId=VAR_010723.
P -> Q (IN OBESITY).
                                                                                                                                                                                                  MISSING (IN ISOFORM P -> A.
                                                   ¥
                                                                                                                                                                                                                               LIGAND-BINDING (POTENTIAL) PHOSPHORYLATION (BY MAPK)
                                                            /FTId=VAR_010728
                                                                                                     LIGAND-BINDING).
/FTId=VAR_010726
                                                                                                                          R -> H (IN COLON
                                                                                                                                                BINDING
                                                                                                                                    /FTId=VAR_010725
                                                                                                                                                                                                                                                                                            Disease mutation; Diabetes mellitus;
                                                 '
                                      IA (IN REF. 3 AND 4).
IA (IN REF. 3 AND 3).
                                                                                                                                                         (IN COLON CANCER;
                                                                                                                                                                                                                                                                                                               Activator; DNA-binding;
                                                                                                                                                                                                                                                                        RECEPTOR-TYPE
                                                                                                                          CANCER;
                                                                                                                                                       SSOT
                                                                                                                          PARTIAL LOSS
                                                                                                                                                                                                                                (BY
                                                                                                                                                         QF
                                                                                                                                                                                                                                                                                                     splicing;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 443; Conser
                                                                                                                                                                                                                                                                                                                 PPAT_MACMU STANDAKU;

PPAT_MACMU STANDAKU;

018924; Q9TQW6;

16-CCT-2001 (Rel. 40, Created)

16-CCT-2001 (Rel. 40, Last sequence update)

16-CCT-2001 (Rel. 40, Last annotation update)

16-CCT-2001 (Rel. 40, Last annotation update)
diabetes and hyperinsulinaemia in rhesus monkeys.";

Int. J. Obes. Relat. Metab. Disord. 22:1000-1010(1998).

-- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIFIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.

-- SUBGULT: HETERODIMER WITH THE RETINOID X RECEPTOR.

-- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                          _MACMU
                                                                                                                                                                           TISSUE=Adipose tissue;
MEDLINE=99021153; PubMed=9806316;
Hotta K., Gustafson T.A., Yoshiok
                                                                                                                                                                                                                                                Cercopithecinae; Macaca. NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                      PPARG OR NRIC3.
Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                          Hansen B.C.;
                                                                                                                                           Relationships of PPARgamma and PPARgamma2 mRNA levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQVIKKTETDMSLHPLLQEIYKDLY 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNC
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                                                                                                                                                                                                                     (ISOFORMS 1 AND
                                                                                                                                                                         T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.6%;
                                                                                                                                                                         Yoshioka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2231; DB 1; Pred. No. 1.7e-116;
                                                                                                                                                                                                                                                                             Craniata; Vertebrata;
Catarrhini; Cercopith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                     2).
                                                                                                                                                                        Ortmeyer H.K., Bodkin
                                                                                                                                                                                                                                                                          Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                 (PPAR-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 505;
                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                             ç
                                                                                                                                             obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
Phosphorylation.
DNA_BIND 139
ZN_FING 139
ZN_FING 176
DOMAIN 318
MOD_RES 112
                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000035; Znf_C4
SMART; SM00430; HOLI; 1
SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00308; STRDIOFINGER.
PRINTS; PR00044; STROIDFINGER.
PRODM; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF033103; AAB87480.1; -.
EMBL; AF033343; AAB87482.1; -.
EMBL; AF033342; AAB87481.1; -.
HSSP; P37231; 1FM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transcription regulation; Activator; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
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TISSUE SPECIFICITY: HIGHEST EXPLESION IN ADIPOSE TISSUE.
LIVER, HEART, KIDNEY, STOMACH, DUODENUM AND COLON.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMIL.
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                                                                                                                                                                                                                                                                                                                        MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF
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439; Conser
                                                                                                ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE
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            LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII
                                             LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII
                                                                                                                                                    RIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR
                                                                                                                                                                                                     QLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNC
                                                                                                                                                                                                                                                        DIKPFTTVDFSSISAPHYEDIPFTRTDPMVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
                                                                                                                                                                                                                                                                    DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00031; NUCLEAR_RECEPTOR; 1.
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3; Mismatches
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MISSING (IN ISOFORM 1)
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There are no rest
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062807; 077815;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterisation of porcine peroxisome proliferator-activated receptors gamma 1 and gamma 2: detection of breed and age differences in gene expression.";
Biochem. Biophys. Res. Commun. 249:713-718(1998).

-i- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIFICEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.

-i- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.

-i- SUBCELLULAR LOCATION: Nuclear.

-i- SUBCELLULAR LOCATION: Nuclear.

-i- SUBCELLULAR LOCATION: Nuclear.

-i- SUBCELLULAR LOCATION: Nuclear.
                          EMBL;
                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99410873; PubMed=10481259;
MEDGINE-99410873; PubMed=10481259;
Ding S.T., McNeel R.L., Mersmann H.J.;
"Expression of porcine adipocyte transcripts:
differentiation in vitro and in vivo.";
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MEDLINE-9913654; PubMed-9931452;

HOUSEKNECHT K.L., Bidwell C.A., Portocarrero C.P.,

"Expression and CDNA Cloning of porcine peroxisome activated receptor gamma (PPARgamma).";
                                                                                                                                                                                                                                                                                  This
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                 PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE IN SPLEEN. VERY LOW LEVELS IN KIDNEY, INTESTINE, LUNG ANT SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                          NR1 SUBFAMILY.
                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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AF059245; AAC14348.1;
AF103946; AAD19577.1;
AJ006757; CAA07225.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n in vitro and in vivo.";
Physiol. 123B:307-318(1999).
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                                                                                                                                                                                                                                                                                                                                                                 LEVELS IN KIDNEY, INTESTINE, LUNG AND N TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
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CONFLICT
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DNA_BIND 138
ZN_FING 138
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MOD_RES 111
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PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; Znf_C4Steroid; 1.
SMART; SM00430; HCLI; 1.
SMART; SM00430; HCLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; Activator; DNA-binding; Receptor; Transcription regulation; Activator; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative
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                                                         LSGDRPGLLNVKPIEDTQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
                                                                                                                                                                                    ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE
                                                                                                                                                                                                                                                                              QLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNC
                                                                                                                                                                                                                                                                                                                          DIKPFTTVDFSSISTPHYEDIPFPRADPMVADYKYDLKLQDYQSAIKVEPVSPPYYSEKT
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IPR001723; Stdhrmn_receptor.
IPR001628; Znf_C4steroid.
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R (IN REF. 3)
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RESULT 4

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STANDARD;

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the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vidal-Puig A., Jimenez-Linan M., I
Spiegelman B., Flier J.S., Moller
Regulation of PPAR gamma gene exp
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TISSUE-Addipose tissue;
MEDLINE-95011536; PubMed-7926726;
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Mammalia; Eutheria;
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MEDLINE=96249427; PubMed=8647948;
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                                                                                                                                                                                                                                                                                                HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PRROXISOMAL BETA-COXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS. SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR. SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 AND 2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE. ALSO
                                                                                                                                                                                                                    DEVELOPMENTAL STAGE:
AND INCREASES UNTIL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH
                                                                                                                                                                              NR1 SUBFAMILY.
                                                                                                                                                                                                SIMILARITY: BELONGS
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                                                                                                         SWISS-PROT entry is copyright. It is produ
sen the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alvares K., Huang Q., Rao M.S., Rec of a new member of the peroxisome gene family from mouse liver."; Chem. 268:26817-26820(1993).
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57BL/6 X CBA;
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BA; TISSUE=Liver;
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Sciurognathi;
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regulator of an
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                        (See http://www.isb-sib.ch/announce/
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adipocyte enhancer.";
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Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
Prom; PR00398; STRDHORMONER.
PRINTS; PR00043; STRDHORMONER.
ProDom; PD000035; Znf_C4steroid; 1
SMART; SM00430; HOLT; 1.
SMART; SM00399; ZnF_C4; 1.
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Receptor; Transcription regulation; Ac
Nuclear protein; Zinc-finger; Multiger
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MGD; MGI:97747; Pparg.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
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EMBL; U01664; AAA62110.1;
EMBL; U01841; AAC52134.1;
EMBL; U10374; AAA19971.1;
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 LQVIKKTETDMSLHPLLQEIYKDLY
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84.0%;
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Pred. No. 3
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NSL -> SSF (IN REF. 2).

N -> S (IN REF. 2 AND 4

L -> F (IN REF. 2).
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088275; 090WG0; Q9R197;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                     PHÓSPHORYLATION OF SER-112, AND MUTAGENESIS OF SER-112.

MEDLINE-97184167; PubMed-9030579;
Adams M., Reginato M.J., Shao D., Lazar M.A., Chatterjee V.K.;
"Transcriptional activation by peroxisome proliferator-activated receptor gamma is inhibited by phosphorylation at a consensus mitogen-activated protein kinase site.";
J. Biol. Chem. 272:5128-5132(1997).
                                                                                                                                                                                                                         Science [7]
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Hu E., Kim J.B., Sarraf P., Spiegelman B.
"Inhibition of adipogenesis through MAP k
phosphorylation of PPARgamma.";
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 phosphorylation and
                             Zhang B., Berger J., Zhou G., Elbrecht A., Biswas White-Carrington S., Szalkowski D., Moller D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley; TISSUE-Adipose tissue; Tanaka T., Itoh H.; Tanaka T., Itoh H.; "Down regulation of PPAR gammma."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
STRAIN-Sprague-Dawley; TISSUE-Brown adipose tissue.
MEDLINE-99367468; PubMed-10438514;
                                                           MEDLINE=97112959; PubMed=8943212;
                                                                                                                                                                                                                                                                                                                             "Photoreceptor phagocytosis selectively in retinal pigment epithelial cells."; J. Neurosci. Res. 60:328-337(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miyakita A., Okuno S., Watanabe T.K., Oga K., Suto T., Nakagawa K., Nakahara Y., Higashi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peroxisome proliferator activated PPARG OR NRIC3.
                                                                                                                                                                                                                                                                                                                                                                                           Ershov A.V., Bazan N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Long Evans;
MEDLINE-20259576; PubMed-10797535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM Escher P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                               PHOSPHORYLATION
                                                                                               <u>@</u>
                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning of rat PPAR-gamma Submitted (FEB-1998) to the EMBL/GenF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Adipocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHVIKKTETDMSLHPLLQEIYKDLY 505
                                                                                                                                                                                                                                      274:2100-2103(1996).
and mitogen-activated protein kinase-mediated lation and activation of peroxisome proliferato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JAN-2001) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                   kinase-mediated
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proliferator-activated
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation.
DNA_BIND 139
ZN_FING 139
ZN_FING 176
DOMAIN 318
MOD_RES 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor gamma.";

J. Biol. Chem. 271:31771-31774(1996).

J. Biol. Chem. 271:31771-31774(1996).

-i-FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PARHWAY OF FATTY ACIDS. KEY REGULATOR OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMBOSTASIS.
                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
MUTAGEN
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00031; NUCLEAR_RECEPTOR; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00430; HOLI; 1
SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00104; hormone_rec;
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF246458; AAF63386.1; HSSP; P37231; 1FM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE.
PTM: PHOSPHORYLATED BY MAPK. THE PHOSPHORYLATION INHIBITS
PPAR GAMMA ACTIVITY.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR. SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 AND 2
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                                                                                                                                                                  MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF
    OLYN
                                                                      DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
                                                DIKPFTTVDFSSISAPHYEDIPFTRADPMVADYKYDLKLQEYQSAIKVEPASPPYYSEKT
                                                                                                                                            {\tt MGETLGDPPVDPEHGAFADALPMSTSQEITMVDTEMPFWPTNFGISSVDLSVMDDHSHSF}
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000536; Hormone_rec_lig.
IPR001723; Stdhrmn_receptor.
IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                  505
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                                                                                                                                                                                                                                        Conservative
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83.8%;
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No. 6.4e-112;
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S->A: IN
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                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY MAPK) SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene
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                                                                                                                                                                                                                                      Mismatches
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Activator; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY
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CC PEROXISOMAL BETA-OXIDATION NUCLEAR.

CC PEROXISOMAL BETA-OXIDATION NUCLEAR.

CC OF ADIPOCYTE DIFFERNATIVE SPLICING.

CC OT ALTERNATIVE PRODUCTS IN THE RECEPTOR.

CC OT ARE PRODUCTS AND ACTIVATES TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES TO A PROMOTER ELEMENT ACHDS. KEY REGULATOR CC OF ADIPOCYTE DIFFERENTIATION PATHWAY OF FATTY ACIDS. KEY REGULATOR CC OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMBOSTASIS.

CC -1- SUBCULTIAR LOCATION: NUCLEAR.

CC -1- SUBCULTIAR LOCATION: NUCLEAR.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 AND 2 (SHOWN HERE);

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE. LOWER IN COLORER AND CHARLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAT BOVIN STANDARD;

PPAT BOVIN STANDARD;

018971;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98042483; PubMed=9367859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPARG OR NR1C3
Bos taurus (Bo
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DETECTED IN OVARY MAMMARY GLAND
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                                                                                                                                                                                                                                                                           NUCLEAR HORMONE RECEPTOR FAMILY.
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                                                                                                                                                      collaboration -
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Best Local
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ZN_FING
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PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation.
DNA_BIND 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Transcription regulation; Activator; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
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InterPro; IPR001723;
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                                                                                                               LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
                                                                      LQVIKKTETDMSLHPLLQEIYKDLY
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                                                             LQVIKKTETDMSLHPLLQEIYKDLY
                                                                                                   LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
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Y12419; CAA73032.1;
P37231; 1FM9.
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SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                         -NRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR
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83.6%;
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Stdhrmn_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGAND-BINDING (POTENTIAL).
PHOSPHORYLATION (BY MAPK) (
SIMILARITY).
MISSING (IN ISOFORM 1).
MSSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2132; DB 1
Pred. No. 4.9e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR RECEPTOR-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
N (BY MAPK)
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Best Local
                                                                                                                                                                                                              DNA_BIND
ZN_FING
ZN_FING
DOMAIN
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between
the Euro
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00104; hormone_rec; 1. pfam; pF00105; zf-C4; 1. PRINTS; PR00398; STRDHORMONER. PRINTS; PR00047; STROIDFINGER. ProDom; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a licence agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aperlo C., Pognonec P., Saladin R., Auwerx J., Boulukos K.E., "cDNA cloning and characterization of the transcriptional act of the hamster peroxisome proliferator-activated receptor hap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus griseus (Chinese hamster).
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z30972; CAA83219.1; -. HSSP; P37231; 1FM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96032361; PubMed=7557447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cricetulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                         Nuclear
                                                                                                                                                                                                                                                                                     Receptor;
61
                          91
                                                      بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR. SUBCELULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.
                                                   MVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162:297-302(1995).
FUNCTION: RECEPTOR THAT
ADYKYDLKLQEYQSAIKVEPASPPYYSEKAQLYNRPHEEPSNSLMAIECRVCGDKASGFH
                         ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYN-----
                                                                                                             403;
                                                                                                                                                                                                                                                                                                                SM00430; HOLI; 1
SM00399; ZnF_C4;
                                                                                                                                                                                                                                                       protein;
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY.
                                                                                                                                                                                                                                                   PS00031; NUCLEAR_RECEPTOR; 1.
7; Transcription regulation; Activator; DNA-binding; protein; Zinc-finger; Multigene family; Phosphoryla NUCLEAR RECEPTOR-TYPE.
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                                                                                                             Conservative
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                                                                                                                                                                    54472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                           58.2%;
84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
or activated receptor ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                            6;
                                                                                                                                      Score
                                                                                                          Pred. No. 3.70; Mismatches
                                                                                                                                                                                               LIGAND-BINDING (PHOSPHORYLATION
                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                    BBDCA0704F837ADB
                                                                                                                           2043;
No. 3
                                                                                                         3.7e-106;
hes 4;
                                                                                                                                        DB 1;
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                                                                                                                                                                                                               (POTENTIAL)
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                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                     Phosphorylation
                                                                                                                                      Length 475;
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InterPro; InterPro;

InterPro;

EMBL; or send

U84893; AAB96380.1; P37231; 1FM9.

an email to license@isb-sib.ch).

Pfam;

PF00104; hormone\_rec;

IPR000536; Hormone\_rec\_lig.
IPR001723; Stdhrmn\_receptor
IPR001628; Znf\_C4steroid.

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Usage its content

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                       induced during cyclic adenosine monophosphate-stimulated differentiation of alveolar type II pneumonocytes."; Endocrinology 138,3695-3703(1997).

-I- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR OF ADDICOVER BUTTATION AND GLUCOSE HOMEOSTASIS.
-I- SUBCULLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPAT_RABIT
019052;
                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, East annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                        Michael L.F., Lazar M.A., Mendelson C.R.; "Peroxisome proliferator-activated receptor gammal expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97418978; PubMed=9275054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
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                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced the ween the Swiss Institute of Bioinformatics and terropean Bioinformatics Institute. There are no
                                                                                                                                                                                                                                 SIMILARITY:
NR1 SUBFAMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNHPESSQLFAKVLQKMTDLRQIVTEHVQLLHVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I PGF I NLDLNDQVTLLKYGVHEI I YTMLASLMNKDGVLI SEGQGFMTREFLKSLRKPFGD
                                                                                                                                                                                                                                 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zealand white;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                BELONGS TO
                                                                                                                                                                                                                                                THE NUCLEAR HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RNKCQYCRFQKCLAVGMSHNAIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leporidae; Oryctolagus
                                                                                                                                                                                                  It is produced through
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                                                                                                                                                                                         a collaboration -
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Best Local S
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                                                                                                                             PART XENLA STANDARD,
P37234;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40 activated receptor gamma
                                                                                                                                                                                                                     _XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
ZN_FING
ZN_FING
DOMAIN
           Dreyer C., Krey G., Keller H., Givel F., Hu "Control of the peroxisomal beta-oxidation
                                                                                                                  Peroxisome proliferator activated re PPARG OR NRIC3.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000035; Znf_C4steroid; 1.

SMART; SM00430; HOLI; 1.

SMART; SM0039; Znf_C4; 1.

SMART; SM00399; Znf_C4; 1.

PROSITE; PS000031; NuCLEAR_RECEPTOR; 1.

Receptor; Transcription regulation; Activator; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Phosphoryla DNA_BIND 109 173 NUCLEAR RECEPTOR-TYPE.
                              SEQUENCE FROM N.A.
MEDLINE=92191267; PubMed=1312391;
                                                                                              Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
                                                                   xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00398; STRDHORMONER PRINTS; PR00047; STROIDFINGER.
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                                                                                                                                                                                                                                                                              LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYN-------
                                                                                                                                                                                                                                                                 LNHPEASQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RNKCQYCRFQKCLAVGMSHNAIRF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKTHEEPSNSLMAIECRVCSDKASGFH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVDTEMPFWPTNFGIGSVDLSVMDDHSHSFDIKPFTTVDFSSISAPHYEDLPFARADPMV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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109
146
288
82
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receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
129
168
475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.2%;
84.8%;
                                                                                              Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2041;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
FA2688295310D9E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGAND-BINDING (POTENTIAL) PHOSPHORYLATION (BY MAPK)
                                                                                                          Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                         Vertebrata; Euteleostomi;
                      Helftenbein G., Wahli W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
          pathway
                                                                                              Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation.
                                                                                                                                           (PPAR-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 475;
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           novel family
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                                                                                                                                                                                                                                                                                                                420
                                                                                                                                                                                                                                                                                                                                      388
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Best Local S
Matches 307
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ZN_FING
ZN_FING
DOMAIN
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PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; C42214; C42214.
HSSP; P37231; 1FM9.
TRANSFAC; T01354; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krey G., |
Wahli W.;
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                   Receptor;
Nuclear p
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00104; hormone_rec; 1. Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of sicinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                        PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M84163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94100165; PubMed=8274443; Krey G., Keller H., Mahfoudi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 68:879-887(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Xenopus peroxisome proliferator activated receptors:
                        120
 144
                                                                                                                                            31
                                                                      60
                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NR1 SUBFAMILY.
                                                                                                                                           MVDTEMPFWPT-NFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIP-----FT
 NAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAIL
                                                                                                                     MVDTEMPFWSNLNFGMNSMDMSALEDHCQPYDIKPFTTVDFSSINS-HYDDILDEKTFLC
                       ASGFHYGVHACEGCKGFFRRTIRLKLIYERCDLNCRIHKKSRNKCQFCRFQKCLAVGMSH
                                                                     RNDQSPIDYKYDLKLQECQSSIKLEPPSPPYFSDKPQCSKAFEDTPNSFIAIECRVCGDK 119
                                                                                             RTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQ-----
                                                                                                                                                                    al Similarity
307; Conser
                                                                                                                                                                                                                                                                                    r; Transcription regulation; Activator; DNA-binding; protein; Zinc-finger; Multigene family; Phosphorylation 113 177 NICLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                   477
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113
150
293
87
                                                                                                                                                                    Conservative
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133
172
477
87
                                                                                                                                                                                                                  54055 MW;
                                                                                                                                                                              41.9%;
62.7%;
                                                                                                                                                                    44;
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                                                                                                                                                                              Score
Pred.
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                                                                                                                                                                                                                                                    LIGAND-BINDING
                                                ----Y----
                                                                                                                                                                                                                  160F87A401CB7246 CRC64;
                                                                                                                                                                   Mismatches
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No. 1
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                                                                                                                                                                               .5e-74;
                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                    (POTENTIAL)
                                            -NRNKCQYCRFQKCLAVGMSH
                                                                                                                                                                    49;
                                                                                                                                                                                         Length 477;
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                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                 Gaps
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There

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RESULT 10
PPAS_HUMAN
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                                                                                                                                                            MEDLING-...

Skogsberg J., Kannisco...

Skogsberg J., Kannisco...

Larsson C., Ehrenborg E.;

"Characterization of the human peroxisome
"Characterization of the human peroxisome
receptor delta gene and its expression.";

mol. Med. 6:73-81(2000).
                                                                                                                                                                                                                                                                                                  MEDLINE-93078797; PubMed=1333051; MEDLINE-93078797, Rutledge S.J.,
                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peroxisome proliferator activated receptor beta (PPAR-beta)
(PPAR-delta) (Nuclear hormone receptor 1) (NUC1) (NUCI).
PPARB OR NRIC2 OR PPARD.
                                                                                                                                                                                                                                                                                                                                                                                                                               Q03181;
01-OCT-1993
            This
                                                                                                                                                                                                                                                                       "Identification of superfamily that
                                                                                                                                                                                                              MEDLINE=20311491; PubMed=10851270; Skogsberg J., Kannisto K., Roshani
                                                                                                                                                                                                                                                                                            Schmidt A.,
Rodan G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPAS_HUMAN
                                                                                                                                               Phillips S.;
                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                     nitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
                                                         SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: UBIQUITOUS WITH MAXIMAL LEVEL.
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8 LLQEIYKDLY 477
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SMART; SM00430; HOLI; 1
SMART; SM00399; ZnF_C4;
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Pfam; PF00105; zf-C4; 1
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HSSP; P03372; 1HCO.
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EMBL; AF246301; AAF62553.1;
EMBL; AF246302; AAF62553.1;
EMBL; AL022721; CAB38629.1;
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EMBL; AF246303; AAF62553.1;
EMBL; AF246299; AAF62553.1;
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TRANSFAC; T02745; -
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                LLQVIKKTETDMSLHPLLQEIYKDLY 443
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D 74 138 NUCLEAR RECEPTOR-TYPE.
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IPR001723; Stdhrmn_receptor.
IPR001628; Znf_C4steroid.
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InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
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-i- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS PUNCTION: RECEPTOR AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
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HSSP; P03372; 1HCQ.
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or send an email to license@isb-sib.ch).
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Endocrinology 137-4400 (700-201)
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                                                                                                                                                                                                                                                                                                                                                                  Nuclear
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TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY
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ev A., Siegrist-Kaiser C.A.,
W.W., Meier C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
                                                                                            DSPIDP----ESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDI 62
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                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                       Zinc-finger; Multigene family; Pho
166 NUCLEAR RECEPTOR-TYPE
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49.2%; Pred. No. 1.40
tive 70; Mismatches
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C4-TYPE.
LIGAND-BINDING (POTENTIAL).
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Sciurognathi; Muridae;
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; Murinae; Rat
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PPAR_MOUSE
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                            Jones P.S., Savory R., Barratt P., Bell A.R., Gray T.J.B. Jenkins N.A., Gilbert D.J., Copeland N.G., Bell D.R.; "Chromosomal localisation, inducibility, tissue-specific and strain differences in three murine peroxisome-proliferator-activated-receptor genes."; Bur J. Blochem. 233:219-226(195).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Peroxisome proliferator activated receptor
PPARA OR NRIC1 OR PPAR.
                                                                                                                            STRAIN=Swiss Webster; TISSUE=Live
MEDLINE=96061953; PubMed=7588749;
                                                                                                                                                                                         Biochem.
                                                                                                                                                                                                        Gearing K.L., Crickmore A., Gustafsson J.-A.;
"Structure of the mouse peroxisome proliferator activated receptor
alpha gene.";
                                                                                                                                                                                                                                                 MEDLINE=94168583; PubMed=8123021;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             by peroxisome proliferato
Nature 347:645-650(1990).
                                                                                                                                                                                                                                                                                                                                     Issemann I., Green S.;
"Activation of a member of the steroid
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 FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SHYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FO
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Sciurognathi; Muridae;
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Bell D.R.;
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EMBL; X75289; CAA53042.1; JOINED.
EMBL; X75290; CAA53042.1; JOINED.
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EMBL; X75292; CAA53042.1; JOINED.
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EMBL; X75294; CAA61754.1; -.
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ZN_FING
ZN_FING
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Nuclear p
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InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, KIDNEY AND HEART. VERY WEAKLY EXPRESSED IN BRAIN AND TESTIS.
DEVELOPMENTAL STAGE: IT APPEARS FIRST AT DAY 13.5 POSTCONCEPTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
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                                                                                        ADYQYLGSCPGSEGSVITDTLSPASSPSSVSCPVI---PASTD-----ESPGSALNIE 101
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LAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHLYDSYIKSFPLT
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236; Conser
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                                                                                                                                                                                                                                                                                                                                                        protein;
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PS00031; NUCLEAR_RECEPTOR; 1.
Transcription regulation; Activator; DNA-binding;
protein; Zinc-finger; Multigene family.
protein; 2166
NUCLEAR_RECEPTOR-TYPE.
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nilarity 48.4%;
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C4-TYPE.
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P35396; P37239;
O1-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
30-MAY-2000 (Rel. 3
                               Peroxisome proliferator activated receptor beta (PPAR-beta) (PPAR-delta) (Nuclear hormone receptor 1) (NUC1). PPARB OR NRIC2 OR PPARD.
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                                                                                                                                                                 STRAIN=BALB/c;
                                                                                                                                                                                                  "Differential expression and activation of a family peroxisome proliferator-activated receptors."; Proc. Natl. Acad. Sci. U.S.A. 91:7355-7359(1994).
                                                                                                                                                                                                                                     Kliewer S.A., Forman B.M., Blumberg B., Mangelsdorf D.J., Umesono K., Evans R.M.
                                                                                                                                                                                                                                                                                                                         acids in preadipocytes. Homology to
                                                                                                                                                                                                                                                                                                                                          Amri E.-Z., Bonino F., Ailhaud G., Abumrad N.A., Grimaldi P.A.; "Cloning of a protein that mediates transcriptional effects of fatty
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Adipocyte; MEDLINE=95138211; PubMed=7836471;
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                            SEQUENCE OF 1-145 FROM
                                                                                                                                                                                                                                                           MEDLINE=94316694; PubMed=8041794;
                                                                                                                                                                                                                                                                         TISSUE=Liver
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                      receptors
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           SUBCELLULAR LOCATION: Nuclear. TISSUE SPECIFICITY: HEART, ADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEIYRDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEIYKDLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFLKNLRKPFCDIMEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNIGYIEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443
                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                         270:2367-2371(1995).
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BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29, Created)29, Last sequence update)39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                            Sciurognathi; Muridae; Murinae; Mus.
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NUCLEAR
            ADRENAL
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HORMONE RECEPTOR FAMILY
            AND INTESTINE
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PPARA OR NR1C1

OR PPAR.

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PPAR_HUMAN
ID PPAR_H
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AC 01-OCT
DT 15-JUL
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DE Peroxi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
007869; Q92689; Q16241; Q92486; Q9Y3N1;
01-0CT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peroxisome proliferator activated receptor al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00398; STRDHORMONER. PRINTS; PR00047; STROIDFINGER. ProDom; PD000035; Znf_C4steroi
                                                                           PPAR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00430; HOLI; SMART; SM00399; ZnF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
Receptor: Transcription regulation; Activator; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:101884; Ppard
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                                                                                                                                                     415
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                                                                                                                                                                                                                                                                                         SLMNKDGVLISEGQGFMTREFLKSLRKPEGDFMEPKFEFAVKFNALELDDSDLAIFIAVI
                                                                                                                                                                                                                                                                                                                                                                                                                 RALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQ :| :||:|::|: :| ; :| ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTQLYNRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADL 177
                                                                                                                                                    MMQWLKKTESETLLHPLLQEIYKDMY
                                                                                                                                                                                 LLQVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                              ILCGDRPGLMNVPQVEAIQDTILRALEFHLQVNHPDSQYLFPKLLQKMADLRQLVTEHAQ
                                                                                                                                                                                                                            ILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQ
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                                                                                                                                                                                                                                                                                                                                    PPYNEISVHVFYRCQSTTVETVRELTEFAKNIPNFSSLFLNDQVTLLKYGVHEAIFAMLA
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PF00105; zf-C4; 1
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P03372; 1HCQ.
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U10375; AAA19972.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Zinc-finger; Multigene family.

D 73 137 NUCLEAR RECEPTOR-TYPE.

73 93 C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
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                                                                           STANDARD;
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EA -> DG (IN REF. 2).
; 58E0F595DD193FDA CRC64;
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Pred. No. 3.9
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.9e-53;
 alpha
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 (PPAR-alpha).
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RA Dunham 1., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Ra Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Ra Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Ra Birdy C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Ra Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clay S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clay S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clay S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clay S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clay S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clay S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Ra Clay S.M., Cobley S.M., Fleming K., French L., Garner A.A., King A., Ra Laird G.K., Langford G.F., Leversha M.A., Lloyd C., Lloyd D.M., Ra Hall R.E., Jones M.C., Kershaw J., Kinberley A.M., King A., Ra Hall R.E., Jones M.C., Kershaw J., Kinberley A.M., King A., Ra Hall G.K., Langford G.F., Leversha M.A., Lloyd C., Lloyd D.M., Ra Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T., Ra Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T., Ra McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T., Ra McClay J., McLaren S., Kuce C.D., Smalley S., Smith M.L., Ross M.T., Schott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Ross M.T., Schott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Ross M.T., Steward C.A., Pasarson D.J., Milner T.E., Wilming L., Milliams L., Williams S.A., Williams S., Kuds K., King A., Williams S., Kuds K., King A., Williams S., Kuds K., Seski T., Asakawa S., Kudoh J., Shimizu N., Mince S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Ra Maright A., Shiman D., Song L., Wang S., Wang S.
   Nature
                           Tilahun Y., Wright H.; "The DNA sequence of human chromosome Nature 402:489-495(1999).
                                                                                           Wilkinson P., Boder
Tilahun Y., Wright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20057165; PubMed=10591208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95071923; PubMed=7981125;
Mukherjee R., Jow L., Noonan D., McDonnell D.P.;
"Human and rat peroxisome proliferator activated receptors (PPARs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93277839; PubMed=7684926;
Sher T., Yi H.F., McBride O.W., Gon
"cDNA cloning, chromosomal mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         demonstrate similar tissue distribution but different
to PPAR activators.";
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
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PRINTS; PRO0047; STROIDFINGER.
PRODOM; PD0000035; Znf_C4Sterroid;
SMART; SM00430; HOLI; 1.
SMART; SM00430; ZnF_C4; 1.
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InterPro; IPR001723;
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SUBBURIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: SKELETAL MUSCLE, LIVER, HEART AND KIDNEY.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
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                                                               MPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTD
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                                       MPRSEKAKLKAEILTCEHDIEDSETADLKSLAKRIYEAYLKNFNMNKVKARVILSGKASN
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PF00105; zf-C4; 1.
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A -> V (IN REF. 1).
G -> A (IN REF. 2).
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(See http://www.isb-sib.ch/announce/

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EMBL; M84161; AAA49935.1; PIR; A42214; A42214.

TRANSFAC;

P03372; 1HCQ. FAC; T01352;

InterPro;

IPR000536; IPR001723;

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                                                                                                                                                                                                                                                                                                                                                                                                              "Xenopus peroxisome proliferator activated receptors: genomic organization, response element recognition, heterodimer formation with retinoid X receptor and activation by fatty acids.";

J. Steroid Biochem. Mol. Biol. 47:65-73(1993).

-!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell
[2]
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MEDLINE=92191267; PubMed=1312391;
Dreyer C., Krey G., Keller H., Gi
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01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Peroxisome proliferator activated receptor alpha (PPAR-alpha).
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MEDLINE=94100165; PubMed=8274443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krey G., Keller
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NCBI_TaxID=8355;
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ll 68:879-887(1992).
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SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
SUBCULTULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: UBIQUITOUS.
DEVELOPMENTAL STAGE: OCCYTES, EMBRYOS, AND ADULTS.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
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R PRINTS; PRO0398; STROHOFINGER.
R PODOM; PD000035; Znf_C4steroid; 1.
R SMART; SM00430; HOLL; 1.
R SMART; SM00399; ZnF_C4; 1.
R PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
R PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
W Nuclear protein; Zinc-finger; Multigene family.
W Nuclear protein; Zinc-finger; Multigene family.
T DNA_BIND 109 173 NUCLEAR RECEPTOR-TYPE.
T DNA_BIND 109 173 C4-TYPE.
T ZN_FING 146 168 C4-TYPE.
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C;Superfamily: unassigned erbA-related proteins; erbi
F;136-422/Domain: erbA transforming protein homology
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C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
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                                                                                                             QSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLAS
                                                                                                                                                                      ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE
                                                                                                                                                                                                                    RIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR
                                                                                                                                                                                                                                                                                                                  QLYN----
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                                                                                           QSKEVAIRIFQGCQFRSVEAVQEITEYAKNIPGFVNLDLNDQVTLLKYGVHEIIYTMLAS
                                                                                                                                                       ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE
                                                                                                                                                                                                                                                                                QLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNC
                                                                                                                                                                                                                                                                                                                                             DIKPFTTVDFSSISTPHYEDIPFPRADPMVADYKYDLKLQDYQSAIKVEPVSPPYYSEKT 119
                                                                                                                                                                                                                                                                                                                                                                                                       MGETLGDSLIDPESDAF-DTLSANISQEVTMVDTEMPFWPTNFGISSVDLSVMDDHSHSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
                                                                                                                                                                                                                                                    -----RNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQVIKKTETDMSLHPLLQEIYKDLY 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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85.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2160.5; DB 2
Pred. No. 7.7e-113;
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MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF 60

Indels

62;

Gaps

1;

Matches

Conservative

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R;Zhu, Y.; Alvares, K.; Huang, Q.; Rao, M.S.; Reddy, J.K.
J. Biol. Chem. 268, 26817-26820, 1993
A;Title: Cloning of a new member of the peroxisome proliferator-activated A;Reference number: A49294; MUID:94086482; PMID:8262913
A;Accession: A49294
                                                                                                                                                                                                          A;Description: transcription regulation of adipogenesis; activates transcription in A;Note: binding of the heterodimer to its recognition element induces DNA bending C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Keywords: DNA binding; heterodimer; nucleus; receptor; transcription regulation; z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: liver R; Chen, F.; Law, S.W.; O'Malley, B.W. R; Chen, Biophys. Res. Commun. 196, 671-677, 1993 Biochem. Biophys. Res. Commun. 196, 671-677, 1993 A; Title: Identification of two mPPAR related receptors A; Reference number: JN0881; MUID:94059089; PMID:8240342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Differential expression and activation of a family A;Reference number: A57740; MUID:94316694; PMID:8041794 A;Accession: A57740
                                                                                                                                                                                                                                                                                                                        C; Complex: heterodimer; peroxisome proliferator-activated receptor C; Function:
                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: adipose tissue
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 66-85; 146-160 < TOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Adipocyte-specific A;Reference number: $53748; A;Accession: $53748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Tontonoz, P.; Graves, R.A.; Budavari
Nucleic Acids Res. 22, 5628-5634, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 31-212, 'DR'
A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 31-505 <ZHU>
A;Cross-references: GB:U01841; NID:g454000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Molecule type: mRNA
A:Residues: 31-382,'S',384-505 <KLI>
A:Cross-references: CB:U10374; NID:g507776;
A:Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kliewer, S.A.; Forman, B.M.; Blumberg, B.; Ong, Proc. Natl. Acad. Sci. U.S.A. 91, 7355-7359, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-505 < TON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: mPPARgamma2: tissue-specific regulator of an adipocyte A; Reference number: A54101; MUID:95011536; PMID:7926726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Tontonoz, P.; Hu, E.; Graves, R.A.;
Genes Dev. 8, 1224-1234, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peroxisome proliferator-activated receptor gamma mouse C;Species: Mus musculus (house mouse) C;Date: 02-Aug-194 #sequence_revision 02-Aug-1994 #text_change C;Accession: A54101; A57740; A49294; JN0881; S53748
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                                                                                                                                                                F;139-159/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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                                  Query Match
Best Local
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                                  Similarity
                                                                                                                                                                erbA transforming protein homology zinc finger CCCC motif
                                                                                                             DNA binding zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,215-280,'S',282,'F',284-382,'S',384-441,
                                61.4%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor MUID:95140625; PMID:7
                                                                                                             #status predicted CCCC motif
     Score 2153; D
Pred. No. 2e-1
9; Mismatches
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3;
2e-112;
10;
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C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology F;1-505/Product: peroxisome proliferator-activated receptor gamma 2 *status predicted F;31-505/Product: peroxisome proliferator-activated receptor gamma 1 *status predicted F;31-505/Product: peroxisome proliferator-activated receptor gamma 1 *status predicted F;137-423/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:Y12420; NID:g2653405; PIDN:CAA73033.1; PID:e1188692; PID:g2653406 A;Note: the sequences of residues 301-320 and 321-340 are interchanged in the authors' t C;Comment: By ligand activation, this protein regulates the expression of many genes end hondral beta-oxidation, and adipocyte differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                            peroxisome proliferator-activated receptor gamma 2 - bovine C;Species: Bos prinigenius taurus (cattle) C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 24-Sep-1999 C;Accession: JC5777 R;Sundvold, H.; Brzozowska, A.; Lien, S. Blochem. Biophys. Res. Commun. 239, 857-861, 1997 Blochem. Biophys. Res. Commun. 239, 857-861, 1997 A;Reference number: JC5777; MUID:98042483; PMID:9367859 A;Accession: JC5777
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A;Map position: 22
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A; Residues: 1-505 <SUN>
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                                                                                                                                                             Conservative
                                                                                                                                                                            60.8%;
83.6%;
                                                                                                                                                        Score 2132; DB 2;
Pred. No. 2.9e-111;
                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-475 <APE>
A;Residues: 1-475 <APE>
A;Cross-references: EMBL:Z30972; NID:g461358; PIDN:CAA83219.1; PID:g461359
A;Cross-references: EMBL:Z30972; NID:g461358; PIDN:CAA83219.1; PID:g461359
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: DNA binding; peroxisome; steroid hormone receptor; transcription regulate; 107-393/Domain: erbA transforming protein homology <ERBA>
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ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE
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                                                              DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKN
                                                                              DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS
                                                                                                                                                                                           YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF
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Pred. No. 2
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peroxisome proliferator-activated receptor gamma ch
N;Alternate names: PPAR-gamma
C:Species: Xenopus laevis (African clawed frog)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994
C;Accession: C42214
R;Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helf
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A;Residues: 1-475 <GRI>
A;Cross-references: GB:AJ006758
A;Cross-references: GB:AJ006758
C;Superfamily: unassigned erbA-related proteins;
F;107-393/Domain: erbA transforming protein homol
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A:Title: Characterization of porcine peroxisome
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Pred. No. 3.1e-106;
5; Mismatches 4;
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MOI. Endocrinol. 6, 1634-1641, 1992
A.Title: Identification of a new member of the steroid hormon A:Title: Identification of a new member of the steroid hormon A:Reference number: A45360; MUID:93078797; PMID:1333051
A.Accession: A45360
A.Status: preliminary; not compared with conceptual translating A:Status: preliminary; not compared with conceptual translating A:Status: preliminary; not compared with conceptual translating A:Status: preliminary; not compared with conceptual translating A:Residues: 1-441 <SCH>
A:Residues: 1-441 <SCH
A:Residues: 1-44
                                                                                                                                                                                                                                                                                                                                                                                                           steroid hormone receptor delta - human W,Alternate names: nuclear hormone rece C;Species: Homo sapiens (man) C;Date: 10-dun-1993 #sequence_revision C;Accession: A45360
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A;Status: preliminary; not compared with conceptual translatic A;Molecule type: nucleic acid A;Residues: 1-477 CDRE>
                                                                                                                                                                                                                                                                                                                                                                           R; Schmidt, A.; Endo, N.; Rutledge, S.J.;
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ne receptor; transcription regulation; zinc fin
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A;Residues: 1-468 <GOE>
A;Cross-references: GB:M88592; NID:g206317; PIDN:AAA41918.1; PID:g206318
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein; Reywords: DNA binding; transcription regulation; zinc finger F;100-386/Domain: erbA transforming protein homology <ERBA>
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A;Title: Fatty acids activate a chimera of the clofibric acid-activated receptor A;Reference number: A45288; MUID:92262498; PMID:1316614
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                                                                                                                           YHYGVHACEGCKGFFRRTIRLKLA----YDKCDRSCKIQKKNRNKCQYCRFHKCLSVGMS
                                                                                                                                           YKYDLKLQE----YQSAIKVEPASPPYYSE----KTQLYNRNKCQYCRFQKCLAVGMS 142
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                                                                             HNAIREGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARA 201
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ILAGKTSNNPPFVIHDMETLCMAEKTLVAKMVANGVE-NKEAEVRFFHCCQCMSVETVTE
                             {\tt ILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQE}
                                                              HNAIRFGRMPRSEKAKLKAEILTCEHDLKDSETADLKSLAKRIHEAYLKNFNMNKVKARV
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                                                                                                                                                                                                                                                                                                               31.1%; Score 1091.5; DB 2; 49.2%; Pred. No. 1.7e-53; tive 70; Mismatches 112;
                                                                                                                                                                                                                       TTVDFSSISTPHYEDIPF -- TRTD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1100.5; DB Pred. No. 4.9e-54;
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              ESPICPLSPLEADDLESPLSEEFLQEMG - -
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peroxisome proliferator-activated receptor alpha chain - mouse C;Species: Mus musculus (house mouse) C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change C;Accession: JC2085; S11659; S68199; S67963 R;Gearing, K.L.; Crickmore, A.; Gustafsson, J.A. Blochem. Biophys. Res. Commun. 199, 255-265, 1994 A;Title: Structure of the mouse peroxisome proliferator activate A;Reference number: JC2085; MUID:94186583; PMID:8123021 A;Accession. JC2085
                                                                                                                                                                                                             A:Map position: 15
A:Introns: 70/1; 123/2; 170/1; 237/3; 387/1
C:Superfamily: unassigned erbA-related proteins: erbA transforming protein homology C:Keywords: DNA binding; receptor; transcription regulation; zinc finger F:100-386/Domain: erbA transforming protein homology <FRBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-74, K',76-468 <TSS>
A;Cross-references: GB:X57638; NID:g53764; PIDN:CAA40856.1; PID:g53765
A;Cross-references: GB:X57638; NID:g53764; PIDN:CAA40856.1; PID:g53765
R;Jones, P.S.; Savory, R.; Barratt, P.; Bell, A.R.; Gray, T.J.B.; Jenk.
Eur. J. Biochem. 233, 219-226, 1995
A;Title: Chromosomal localisation, inducibility, tissue-specific expres
A;Reference number: S67963; MUID:96061953; PMID:7588749
A;Accession: S68199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Issemann, I.; Green, S.
Nature 347, 645-650, 1990
A;Title: Activation of a member of the steroid hormone receptor superfamily A;Reference number: S11659; MUID:91015382; PMID:2129546
A;Accession: S11659
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-5 <JOW> C; Comment: This protein r
                                                                                                                                                                         F;102-165/Region: DNA binding F;139-156/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                  A; Gene: PPARalpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S67963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X89577; NID:g1051294; PIDN:A;Experimental source: strain Swiss Webster; tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 413-468 < JON>
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A; Residues: 1-468 <GEA>
                                                                                                                                               ;273-468/Domain: ligand binding #status predicted <LIB>
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                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             protein mediates transcription
                                                                                                                                                                           zinc finger CCCC motif
                                                                       30.9%;
                                                Score 1083.5;
Pred. No. 4.7e
65; Mismatches
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                                                                     1083.5; DB 2;
No. 4.7e-53;
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                                                                                                   468;
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                                                   75;
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A;Residues: 1-148, DG', 151-440 <KLI>
A;Cross-references: GB:U10374; GB:U10375; NID:g507778; PIDN:AAA19972.1;
R;Chen, F.; Law, S.W.; O'Malley, B.W.
Biochem. Biophys. Res. Commun. 196, 671-677, 1993
A;Title: Identification of two mPPAR related receptors and evidence for A;Reference number: JN0881; MUID:94059089; PMID:8240342
A;Accession: PN0676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peroxisome proliferator-activated receptor delta chain - mouse N;Alternate names: peroxisome prolifierator-activated receptor NUC1 C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Sep-1999 C;Accession: I55442; B57740; PN0676 R;Amri, E.Z.; Bonino, F.; Allhaud, G.; Abumrad, N.A.; Grimaldi, P.A. J. Biol. Chem. 270, 2367-2371, 1995 A;Title: Cloning of a protein that mediates transcriptional effects of fatty A;Reference number: I55442; MUID:95138211; PMID:7836471 A;Accession: I55442
A;Experimental source: brain
C;Comment: This protein has function of peroxisome proliferator activated receptor.
C;Comment: This protein has function of peroxisome proliferator activated receptor.
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: DNA binding; hormone receptor; nucleus; zinc finger
F;71-358/Domain: erbA transforming protein homology <ERBA>
F;73-136/Region: DNA binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L28116; NID:g452113; PIDN:AAA63394.1; PID:g452114 R;Kliewer, S.A.; Forman, B.M.; Blumberg, B.; Ong, E.S.; Borgmeyer, U.; Mc Proc. Natl. Acad. Sci. U.S.A. 91, 7355-7359, 1994 A;Title: Differential expression and activation of a family of murine per A;Reference number: A57740; MUID:94316694; PMID:8041794 A;Accession: B57740
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A; Residues: 73-137 <CHE>
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A; Residues: 1-440 < RES>
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A;Gene: ppar delta
C;Superfamily: unassigned erbA-related proteins; erbA transforming
C;Keywords: brain; DNA binding; peroxisome; receptor; zinc finger
F;71-358/Domain: erbA transforming protein homology <ERBA>
F;73-93/Region: zinc finger CCCC mottif
F:110-127/Region: zinc finger CCCC mottif
F:245-440/Domain: ligand binding #status predicted <LIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A) Experimental source: brain
A) Experimental source: brain
C) Comment: This receptor modulates CNS function
C) Comment: This receptor modulates constitution
C) C) Comment: This receptor modulates constitution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 20-Sep-1999 C;Accession: JC4530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:U40064; NID:g1185466; PIDN:AAC52419.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-440 < XIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: JC4530;
A; Accession: JC4530
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C; Species: Rattus norvegicus (Norway rat)
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                                 SLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVI
                                                                                                 PPYNETSVHVFYRCQSTTVETVRELTEFAKNIPNFSSLFLNDQVTLLKYGVHEAIFAMLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1076.5; DB 
Pred. No. 1.1e-52; 
0; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1082.5; DB Pred. No. 4.9e-53;
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C;Superfamily: unassigned erbA-related proteins; erbA transforming
C;Keywords: zinc finger
F;100-386/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Mukherjee, R.; Jow, L.; Noonan, D.; McDonnell, D.P.
J. Steroid Biochem. Mol. Biol. 51, 157-166, 1994
A;Title: Human and rat peroxisome proliferator activated
A;Reference number: 156603; MUID:95071923; PMID:7981125
A;Accession: 156603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peroxisome proliferator activated receptor alpha - human C;Species: Homo sapiens (man) C;Cate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change C;Accession: I56603 R;Mukherjee, R; Jow, L; Noonan, D.; McDonnell, D.P. J. Steroid Biochem. Mol. Biol. 51, 157-166, 1994
c; Species:
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C;Genetics:
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A; Residues: 1-468 < RE
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                                                                                                                                                                                                                                                                                                                            NPPFVIHDMETLCMAEKTLVAK-LVANGIQNKEAEVRIFHCCQCTSVETVTELTEFAKAI
                                                                                                                                                                                                                                                                                                                                                                                                NHPDDIFLFFKLLQKMADLRQLVTEHAQLVQIIKKTESDAALHPLLQEIYRDMY
                                                                                                                         NHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                    MEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKL 389
                                                                                                                                                                                                                                                                           PGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDF
                                                                                                                                                                                                                                                                                                                                               KSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSI
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                                                                                                                                                                                MEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIEKMQEGIVHVLRLHLQS
                                                                                                                                                                                                                                                      PGFANLDLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNGFITREFLKSLRKPFCDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DFSSIS-TPHYEDIPFTRTDPVVADYKYDLKLQEYQS-AIKVE-----PASPPYY- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVDTESPLCPLSPLEAGDLESPLSEEFLQEMGNIQEISQSIGEDSSGSFGFTEYQYLGSC 60
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proliferator-activated Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -468 <RES>
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49.8%;
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                 receptor
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                  human
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A; Dolecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-468 <SHE>
A; Cross-references: GB:L02932; NID:g307340; P
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                 NHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 443
                                                                                                                                                                                                    MEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKL
                                                                                                                                                    PGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDF
NHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKTESDAALHPLLQEIYRDMY
                                                                 MEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIEKMQEGIVHVLRLHLQS
                                                                                                                                    PAFANLDLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNGFITREFLKSLRKPFCDI
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49.8%;
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Pred. No. 1.5
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r residue 33 as Asp
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RESULT 15

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peroxisome proliferator-activated receptor alpha ch N;Alternate names: PPAR-alpha C;Specles: Xenopus laevis (African clawed frog) C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 chain -African clawed

C; Accession: A42214 #text\_change 20-Sep-1999

Cell 68, 879-887, 1992 A;Title: Control of the peroxisomal beta-oxidation pathway A;Reference number: A42214, MUID:92191267; PMID:1312391 A;Accession: A42214 R;Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helftenbein, Cell 68, 879-887, 1992 bу G.; ជ Wahli, W. novel family

of

conceptual translation

A;Status: preliminary; not compared with A;Molecule type: nucleic acid A;Residues: 1-474 <DRE>

A;Cross-references: GB:M84161; NID:g214663; PIDN:AAA49935.1; PID:g214664
A;Note: sequence extracted from NCBI backbone (NCBIP:88292)
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology

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Search completed: February 25, 2003, 04:01:22 Job time: 41 secs
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                                                                                                                                                                                                                                                                                                                                                    Query Match 30.2%; Score 1060.5; DB 2; Length 474; Best Local Similarity 63.5%; Pred. No. 9.1e-52; Matches 207; Conservative 51; Mismatches 65; Indels 3; Gaps
                                                                                                                                                418 LLQVIKKTETDMSLHPLLQEIYKDLY 443
                                                                                                                                                                                                 449 LVQTIKKTETDAALHPLLQEIYRDMY 474
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                                                                                                               358 ILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQ 417
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                                                                                                                               Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/pt
2: /cgn2_6/ptodata/1/pubpaa/pt
3: /cgn2_6/ptodata/1/pubpaa/lt
4: /cgn2_6/ptodata/1/pubpaa/lt
5: /cgn2_6/ptodata/1/pubpaa/lt
6: /cgn2_6/ptodata/1/pubpaa/lt
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Listing first 45 summaries
                /cgn2_6/ptodata/1/pubpaa/US06_NEW_FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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1: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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1125.054 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	% Query Match Length	DB	ID .	Description
1	3508	100.0	889	ا و	US-09-931-007A-1	Sequence 1, Appli
2	2231	63.6	505	10	US-09-765-111A-16	Sequence 16, Appl
ω	2196.5	62.6	506	12	US-10-109-886-6	Sequence 6, Appli
4	2106.5	60.0	811	10	US-09-765-111A-23	23
5	2106.5	60.0	874	10	US-09-765-111A-6	6
6	2099	59.8	777	10	US-09-765-111A-2	2
7	2094	59.7	840	10	US-09-765-111A-4	4
8	2054.5	58.6	478	10	US-09-765-111A-27	27,
9	2054	58.6	475	12	US-10-142-373-2	2, 7
10	1076.5	30.7	440	12	US-10-013-807-2	N
11	524	14.9	121	10	US-09-925-299-1029	
12	512.5	14.6	128	10	US-09-925-299-882	
13	392	11.2	1394	9	US-10-108-605-213	Sequence 213, App
14	385.5	11.0	1237	9	US-10-108-605-211	Sequence 211, App
15	333	9.5	81	10	US-09-864-761-35611	Sequence 35611, A
16	325.5	9.3	448	9	US-09-814-604-2	Sequence 2, Appli
17	325.5	9.3	448	10	US-09-797-727-4	Sequence 4, Appli
18	315	9.0	462	10	US-09-797-727-3	Sequence 3, Appli
19	313	8.9	454	9	US-09-814-604-3	Sequence 3, Appli

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233.5	233.5	252.5	255.5	255.5	255.5	255.5	259.5	260.5	265	266	266	266	266	266	266	270.5	273.5	276.5	276.5	276.5	281.5	282.5	296	312	
6.7	6.7	7.2	7.3	7.3	7.3	7.3	7.4	7.4	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.8	7.9	7.9	7.9	8.0	8.1	8.4	8.9	
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US-09-143-828-4	US-09-143-828-2	US-09-952-559-3	US-09-965-703-59	US-09-965-703-71	US-09-965-703-12	US-09-965-703-11	US-09-965-703-31	US-09-965-703-36	US-09-965-703-63	US-09-042-488B-9	US-09-042-488B-7	US-09-042-488B-5	US-09-965-703-16	US-09-965-703-17	US-09-853-386-42	US-10-013-823-3	US-10-013-823-2	US-09-909-326-2	US-09-909-325-2	US-09-909-446-2	US-10-188-721-1	US-10-155-379-2	US-09-895-840-2	US-09-814-604-1	
Sequence 4, Appli	Sequence 2, Appli	ω	59,	Sequence 71, Appl	Sequence 12, Appl	Sequence 11, Appl	Sequence 31, Appl	Sequence 36, Appl	Sequence 63, Appl	Sequence 9, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 16, Appl	Sequence 17, Appl	Sequence 42, Appl	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	ν	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	N	Sequence 1, Appli	

## ALIGNMENTS

US-09-931-007A-1

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                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc ; LOCATION: (1)...(688) ; LOCATION: (1)...(688) ; OTHER INFORMATION: Sequence for PPAR-gamma-2-gamma-2, a modified human PPAR-gamma ; OTHER INFORMATION: eroxisome Proliferator Activated Receptor-gamma) US-09-931-007A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 688
TYPE: PRT
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APPLICANT: AVENTLS Pharma S.A.
TITLE OF INVENTION: SYSTEM FOR REGULATING IN VIVO THE EXPRESSION OF A TRANSGENE BY
TITLE OF INVENTION: CONDITIONAL INHIBITION
FILE REFERENCE: 03806.0512
CURRENT APPLICATION NUMBER: US/09/931,007A
CURRENT FILING DATE: 2001-08-17
CURRENT FILING DATE: 2001-08-17
                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/239,246 PRIOR FILING DATE: 2000-10-11 NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: FR 00/10730 PRIOR FILING DATE: 2000-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
121 QLYNRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRAL 180
                                                                        61 DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
                                                                                              61 DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
                                                                                                                                                               688;
                                                                                                                                                                                                                                                         100.0%; Score 3508; DB 9; ilarity 100.0%; Pred. No. 6.9e-246; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  Length 688;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
FITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7199/ERP/MAT
CURRENT FILING DATE: 2001-01-18
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 505
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-765-111A-16
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Best Local Sim:
Matches 443;
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                                                                                                                Local Similarity
                                                        1 MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF 60
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                                          {\tt MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF}
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                                                                                                   Conservative
                                                                                                              63.6%;
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                                                                                                Score 2231; DB 10;
Pred. No. 8.6e-154;
0; Mismatches 0;
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	180	121 QLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNC 1	Db	
	124	121 QLYN 1 	Qy	
	120	61 DIKPETTVDFSSISTEHYEDIPETRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT	Db Qq	
	60	1 DIVERGE OF CONDUCTOR OF THE PROPERTY OF THE	Db Db	
	60	IDPESDSTIDTLSANISQEMIMVDTEMPFWPINFGISSVDLSVMEDHSHSF	Qy	
Ν	sq	ery match 62.6%; Score 2196.5; DB 12; Length 506; 1t Local Similarity 86.8%; Pred. No. 2.7e-151; 1ches 439; Conservative 2; Mismatches 2; Indels 63; Gap	Que Bes Mat	
			S	
		LENGTH: 506 TYPE: PRT		
		TWARE: PatentIn version 3.0	; SEQ	
		OR APPLICATION NUMBER: JP231084/1997 OR FILING DATE: 1997-08-27 HER OE STO ID NOS: 10	. ; PR	
		OR APPLICATION NUMBER: PCT/JP98/03734 OR FILING DATE: 1998-08-24	; PR	
		7	; PR	
		RENT APPLICATION NUMBER: US/10/109,886		
			;; FH	
		LICANT: MIZUKAMI, Junko	; AP	
		LICANT: TANABE SEIYAKU CO. LTD. LICANT: TANIGUCHI, Tomoyasu	; AP	
		ence o, Application us/10109886 nt No. US20020119499A1 RAL INFORMATION:	; seq ; pat	
		DS-10-109-886-6	RESUL US-10	
		481 LQVIKKTETDMSLHPLLQEIYKDLY 505	Db	
		419 LQVIKKTETDMSLHPLLQEIYKDLY 443	Qy	
	480	421 LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL	DЪ	
	418	ESSQLFAKLLQKMTDLRQIVTEHVQL	Qy	
	420	361 LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII	Db	
	358	- 14	Qy	
	360	301 QSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHBIIYTMLAS:	Db	
	298	SKEVAIRIFOGCOFRSVEAVOEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLAS	Qy	
	300	241 ALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQE	ДĎ	
	238	- [F]	Qy	
	240	181 RIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR	DЪ	
	178	ESADLR	Qy	
	180		Db	
	124		Qy	
	120	61 DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT :	Db	

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                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47
SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 23
LENGTH: 811
TYPE: PRT
ORGANISM: Homo Sapiens
S-09-765-111A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PARS PPARSGARMA NUCLEIC ACID MOLECULES TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF FILE REFERENCE: B0801/7196/ERP/MAT CURRENT APPLICATION NUMBER: US/09/765,111A CURRENT FILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: US 60/177,109 PRIOR APPLICATION NUMBER: US 60/177,109 PRIOR FILING DATE: 2000-01-20 PRIOR APPLICATION NUMBER: US 60/225,079 PRIOR APPLICATION NUMBER: US 60/225,079 PRIOR PILING DATE: 2000-08-14
    544
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                                                                                                                                                                                                           LLQVIKKTETDMSLHPLLQEIYKDLY 443
                                                                                                                                                                       HSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYS 117
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                                                  LNCRIHKKSRNKCQYCRFQKCLAYGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESA 543
                                                                                                       EKTQLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCD 483
                                                                                                                                                                                                                                                                   425;
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                                                                 --RNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESA 175
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APPLICANT: Kroll, Todd G.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeQ for Windows Version 3.0
SEQ ID NO 6
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US-09-765-111A-6
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APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
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Best Local Similarity
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ORGANISM: Homo
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                                                                                                                               DLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITP 235
               LASLMNKDGVLISEGQGFMTREFLKSLRKPFGDEMEPKFEFAVKFNALELDDSDLAIFIA
                                                                                                                                                                                                  LNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESA
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LASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIA
                                                               LQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTM
                                                                             LQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTM
                                                                                                                                                                                                                                                                   EKTQLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCD 546
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83.7%;
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Pred. No. 1.8e-144;
4; Mismatches 14; I
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US-09-765-111A-2
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PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3
SEQ ID NO 2
LENGTH: 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 77
TYPE: PRT
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                                                                                                                                                                                                                                                                                           QVIKKTETDMSLHPLLQEIYKDLY 443
                                                                                                                                MNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFTAVIIL
                                                                                                                                                                                          SKEVAIRIFQGCQFRSVEAVQEITEYAKSIFGFVNLDLNDQVTLLKYGVHEIIYTMLASL 299
                                                                                                                                                                                                                                                    LAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQ
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QVIKKTETDMSLHPLLQEIYKDLY
                                                                       SGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLL 419
                                                                                                                   MNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIIL
                                                                                                                                                                           SKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKATLTPSNTPLGRNLSTHQTYPVVAEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFD
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                                                         SGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLL
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83.3%;
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Pred. No. 5
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US-09-755-111A-27

; Sequence 27, Application US/09765111A
; Patent NO. US20020106796A1
; GENERAL INFORMATION:
; APPLICANT: Fletcher, Jonathan A.
; APPLICANT: Kroll, Todd G.
; APPLICANT: Kroll, Todd G.
; TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: B0801/7196/ERP/MAT
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US-09-765-111A-4
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APPLICANT: Fletcher, Jonathan A. APPLICANT: Kroll, Todd G.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECU TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF FILE REFERENCE: B0801/7196/ERP/MAT
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                            AKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKP 722
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87.0%;
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Pred. No. 1.3e-143;
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                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10142373 Patent No. US20020137665A1 GENERAL INFORMATION:
                              SOFTWARE: PatentIn
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 47
SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 27
LENGTH: 478
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                                                                                                                                                                                     APPLICANT: EVANS, Ronald
APPLICANT: EVANS, Ronald
APPLICANT: FORMAN, Barry
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR
TITLE OF INVENTION: RECEPTOR-GAMMA,
TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF
FILE REFERENCE: SALK1480-2
                                                             PRIOR APPLICATION NUMBER: US/09/788,070 PRIOR FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: US 09/955,302 PRIOR FILING DATE: 1999-02-22 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/142,373 CURRENT FILING DATE: 2002-05-08
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PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FILING DATE: 2000-08-14
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TYPE: PRT
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86.0%;
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CURRENT APPLICATION NUMBER: US/10/013,807
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,916
PRIOR FILING DATE: 2000-12-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 440
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                                                                      Qγ
                                                                                                                                                              ; TYPE: PRT; ORGANISM: Mus musculus US-10-013-807-2.
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US-10-013-807-2
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                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Guenther, Catherine
APPLICANT: Philips, Russell
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
TITLE OF INVENTION: PROLIFERATOR-ACTIVATED REC
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10013807 Patent No. US20020112256A1
                                                                                                     Matches
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RALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQ 237
                                                          KTQLYNRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMEPKFEFAVKFNALELDDSDLAIF IAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK
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                                                                                                     Conservative
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85.5%;
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62.3%;
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Pred. No. 4.9e-141;
                                                                                                    Score 1076.5; DB 12;
Pred. No. 1.9e-70;
8; Mismatches 64; I
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1029
LENGTH: 121
                                                                                                                                                     RESULT 12
US-09-925-299-882
; Sequence 882, Application US/09925299
; Patent No. US20020055627A1
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; OTHER INFORMATION: Xaa equals any of the naturally occurring;
; NAME/KEY: SITE
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
US-09-925-299-1029
                                                                                                                                                                                                                                                                                      Вp
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                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
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                                    CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
                 PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PA102
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                       522 LNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEP
                                                                                                                                                                                                                                                                                                                                                                                    462 DMNSLAMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLD 521
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                                                                                                                                                                                                                                                                                    LNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGPSFMTREFLKSLRXLLVTLWEP 116
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2000-03-08
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Pred. No. 2.8e-31;
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Best Local S
Matches 98
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SEQ ID NO 213
LENGTH: 1394
TYPE: PRT
                                                                                                                                                                                                                                              Query Match 11.3
Best Local Similarity 27.8
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 213, Application US/10108605
Patent No. US20020160934A1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 882
LENGTH: 128
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 31133B
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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 210
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                                                                                                                                                                                                           48 VDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVV-----ADYKYDLKLQ--
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                                                                                                                                                                           LDSSQLNYLCQKFDEKLDTALSNSSANT------GRNTPAVTANEDADGFFRRSIQQK 433
                                                                                                         IQYRPCTKNQQCS----
                                                                                                                                      -EYQSAIKVEPASPPYYSEKTQLYNRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKL 159
                                   LAA----MQQSTQNRGQQRALATELDDQPRLLAAVLRAHLETCEFTKEKVSAMRQRARDC
                                                                    LAEISSDIDQLNPESADLRALAKHLYD----
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27.8%;
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85.2%;
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Pred. No. 2.6e
80; Mismatches
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US-10-108-605-211
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Best Local :
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SEQ ID NO 211
LENGTH: 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
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APPLICANT: Kamdar, Kim
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NUMBER OF SEQ ID NOS: 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 31133B
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                                                                                                                                                                                           TMLASLMNK--DGVLISEGQGFMTREFLKS-LRKPFGDFMEPKFEFAVKFNALELDDSDL
                                                                                                                                                                                                                                                                       TPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIY 293
                                     IVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLYAWAILTGKTTD----KSP
                                                                                                    AIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQ 410
                                                                                                                                                                                                                                    NPAPELQSE-----QEFSQRFAHVIRGVIDFAGMIPGFQLLTQDDKFTLLKAGLFDALF
                                                                                                                                                                                                                                                                                                                  LDDQPRLLAAVLRAHLETCEFTKEKVSAMRQRARDCPS----YSMPTLLACP-----L
                                                                                                                                                                                                                                                                                                                                                       LYD-----SYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                      NRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKH 183
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                                                                            GLFCAIVLITPDRPGLRNLELIEKMYSRLKGCLQYIVAQNRPDQPEFLAKLLETMPDLRT
                                                                                                                                                          VRLICMFDSSINSIICLNGQ-VMRRDAIQNGANARF--LVDSTFNFAERMNSMNLTDAEI
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/ 29.3%; Pre
/--ive 71;
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Pred. No. 6.4e-20;
1; Mismatches 126;
WSMEDGNNSDGQQNKSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
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US-09-864-761-35611
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SEQ ID NO 35611
LENGTH: 81
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APPLICANT:
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SOFTWARE: Annomax Sequence
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
TYPE: PR
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PRIOR FILING DATE:
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Hanzel, David K.
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               NN: MAP TO NM_007104.1

NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

NN: EXPRESSED IN LUNG, SIGNAL = 1.7

NN: EXPRESSED IN PLACENTA, SIGNAL = 2.4

NN: EXPRESSED IN BRAIN, SIGNAL = 2.7

NN: EXPRESSED IN BRAIN, SIGNAL = 2.7

NN: EXPRESSED IN BT474, SIGNAL = 1.9

NN: EXPRESSED IN HEART, SIGNAL = 3.9

NN: EXPRESSED IN HEART, SIGNAL = 3.9

NN: EXPRESSED IN HEART, SIGNAL = 3.9

NN: EXPRESSED IN HEART, SIGNAL = 4

NN: EXPRESSED IN HELLOO, SIGNAL = 6

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LUE 6.00e-40
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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  February 25, 2003, 03:58:31; Search time 22 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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                    US-09-128-142-4
US-09-114-247a-6
US-09-128-142-20-2
US-08-484-200-2
US-08-188-070-2
US-08-980-115-9
US-08-980-115-9
US-08-980-115-9
US-08-980-115-9
US-08-484-200-4
US-08-484-200-4
US-08-484-200-4
US-08-484-200-4
US-08-484-870-8
US-08-484-870-8
US-08-484-870-8
US-08-484-870-8
US-08-484-870-8
US-08-484-870-8
US-08-33-358-10
US-08-694-501-2
US-08-694-501-3
5223606-2
    US-08-764-870-4
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920.135 Million cell updates/sec
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Patent No.
Patent No.
Sequence
             Sequence 4, Appli
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Sequence 4, Appli
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Sequence 3, Appli
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Qy

1 MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF 60

Query Match 63.6 Best Local Similarity 87.7 Matches 443; Conservative

63.6%;

Score 2231; DB 4; Pred. No. 7.6e-186; 0; Mismatches 0;

Indels 62;

Gaps

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R OF SEQUENCES: 4  SPONDENCE ADDRESS: 4  SPONDENCE ADDRESS: 4  SPONDENCE ADDRESS: 4  ADDRESSE: Jack L. Tribble 57REET: 126 E. Lincoln Ave., P.O. Box 20  STREET: 126 E. Lincoln Ave., P.O. Box 20  CITY: Rahway Jersey COUNTRY: US Jersey 121 . 0765-0907 ZIP: 0765-0907 ZIP: 0765-0907 ZIP: 0765-0907 ZIP: P.O. Box 20  COMPUTER: New Jersey 121 . 0765-0907 ZIP: 1765-0907 ZIP: 0765-0907 Z	1-2 592-383-2 095-728B-4 92-02320A-4 92-02320A-2 92-02320A-2 92-0230A-2 980-115-5 2-9 980-115-5 2-9 333-358-8 463-694-8 463-694-8 463-648A-12 653-648A-12 653-648A-14 466-120-2 GNMENTS	317 9.0 416 4
TVATED R	ent No. 511 quence 2, 1 quence 4, 1 quence 2, 1 quence 5, 1 quence 5, 1 quence 5, 1 quence 8, 1 quence 8, 1 quence 8, 1 quence 1, 1 quence 2, 1	Sequence 4, Appli

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                                                                                                                                                                                                                                     SEQ ID NO 6
LENGTH: 506
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09514247A Patent No. 6365361 GENERAL INFORMATION:
                                                                                                                                                          Matches
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCH; TOMOYASU
APPLICANT: MIZURAMI, JUNKO
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
TITLE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/09/514,247A
CURRENT FILING DATE: 2000-02-28
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                                                                                                                                                                         Local Similarity
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                                               DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
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                              DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT 120
                                                                                         MGETLGDSPIDPESDSTTDTLSANISQEMTMVDTEIAFWPTNFGISSVDLSVMEDHSHSF
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                                                                                                                                                                         62.6%;
86.8%;
                                                                                                                                                    Score 2196.5; DB 4;
Pred. No. 7.6e-183;
                                                                                                                                                                                        DB 4;
                                                                                                                                                         Indels
                                                                                                                                                                                   Length 506;
                                                                                                                                                         63;
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      SEQUENCE DESCRIPTION: SEQ ID NO: US-09-128-142-2
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US-09-128-142-2
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Patent No. 6294559

GENERAL INFORMATION:
APPLICANT: Smith, Roy G.
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
                                                                                                                                     TELEFAX: (908) 59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481
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                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
                                                                                                                                                                                                                                APPLICATION NUMBER: 08/844,007
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/128,142
FILING DATE: 03-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Power Macintosh 7500/100

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Jack L.
                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLQVIKKTETDMSLHPLLQEIYKDLY 443
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                                                                         STRANDEDNESS: single
                                                                                           TYPE: amino acid
                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 126 E. Lincoln
                                                                                                        LENGTH: 477 amino acids
                                                            linear
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                                                                                                                                                         594-4720
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ncoln Ave.,
                                                                                                                                                                                                                     32,633
                                                                                                                                                                                                     <Unknown>
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Qy

29

Matches

Conservative

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Mismatches

Indels

Gaps

1;

Query Match Best Local Similarity

59.5%; 87.0%;

Score 2089; DB 4; Length 477; Pred. No. 1.5e-173;

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US-08-484-200-2
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GENERAL INFORMATION:
APPLICANT: EVANS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: EVANS, RONALD M.
APPLICANT: FORMAN, BARRY M.
APPLICANT: KLLEWER, STEVEN A.
APPLICANT: ONG, ESTELITA S.
TITLE OF INVENTION: NOVEL MEMBERS OF
TITLE OF INVENTION: SUPERFAMILY AND
NUMBER OF SEQUENCES: 6
                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 444 SOUTH FLOWER STATE: LOS ANGELES
STATE: CALTERNAL
CALTE
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//8/484,200
FILLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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619-546-9392
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; ORGANISM: Mus musculus US-08-465-375-2
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                                                                                           SEQ ID NO 2
LENGTH: 475
TYPE: PRT
                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Forman, Barry M.
TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME
TITLE OF INVENTION: PROLIFERATOR ACTIVATED RECEPTOR-GAMMA,
TITLE OF INVENTION: USE THEREOF
 Matches
                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08465375A Patent No. 6022897
                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/465,375A CURRENT FILING DATE: 1995-06-05 EARLIER APPLICATION NUMBER: 08/428,559 EARLIER FILING DATE: 1995-04-25 NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 406;
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TOPOLOGY: linear
MOLECULE TYPE: protein
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 406;
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   Conservative
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                 58.6%;
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85.5%;
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brad. No. 1.7e-170;
Score 2054; DB 3;
Pred. No. 1.7e-170;
4; Mismatches 3;
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RESULT 6
US-09-788-070-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: EVANS, Ronald
APPLICANT: EVANS, Ronald
APPLICANT: EVANS, RONALD
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA,
TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF
FILE REFERENCE: SALK1480-2
CURRENT FILING DATE: US/09/788,070
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/955,302
PRIOR APPLICATION NUMBER: US 09/955,302
PRIOR TILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VETSION 3.0
LENGTH: 475
THE TENT OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                  GRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTT 208
                                                                                                                                                                                                                                                                                                               MVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISAPHYEDIPFTRADPMV 60
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                                                                                                                     YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF
                                                                                                                                                                                                                ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNRPHEEPSNSLMAIECRVCGDKASGFH 120
                                                                                                                                                                                                                                           ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYN------
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85.5%;
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US-08-134-557D-2
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Matches
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human Peroxisome TITLE OF INVENTION: Receptor Gamma:
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121
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TYPE: ami
TOPOLOGY:
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TELEPHONE: 312-616-5460
TO TD NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2 Prud
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                     ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYN---
                                                                                            ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFH 120
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YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF
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Pred. No. 1.1e-169;
2; Mismatches, 2;
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APPLICANT:
APPLICANT:
                                              NFORMATION FOR SEQ ID NO: 10:
            SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acid
                                                                           NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,96
REFERENCE/DOCKET NUMBER: UC.
TELECOMMUNICATION INFORMATION:
                                                                                                                                           APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Apriletti, James APPLICANT: West, Brian TITLE OF INVENTION: Nuclear TITLE OF INVENTION: Binding NUMBER OF SEQUENCES: 16
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                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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STREET: Five Pal
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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             475 amino acids
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Five Palo Alto Square,
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Kushner, Peter J
Apriletti, James W
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                                                              (650)843-5000
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SEQ ID NO 10

475

ORGANISM: Homo FEATURE: LENGTH:

sapiens

EARLIER FILING DATE: 1995-12-13 NUMBER OF SEQ ID NOS: 17 SOFTWARE: PatentIn Ver. 2.0

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GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Fletterick, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Kushner, James W.
APPLICANT: APPLICANT: APPLICANT Brian L.
APPLICANT: Shiau, Andrew K.
APPLICANT: Shiau, Andrew K.
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TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,540
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No. 6266622
NO. TWATIC
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84.8%;
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Pred. No. 1.5e-169;
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LOCATION: (202).
                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/764,870 FILING DATE: 13-DEC-1996
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand TITLE OF INVENTION: Binding Domains
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APPLICANT:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                            COUNTRY: U
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CITY: Palo Alto
CLASSIFICATION:
                                                                                                                                                       STATE:
                                                                                                                                                                                ADDRESSEE: Cooley Godward
STREET: Five Palo Alto Square,
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                                                                                                                                                       CA
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Apriletti, James W
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Baxter, John
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84.8%;
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John D
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Pred. No. 1
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APPLICANT: Apriletti, James W.
APPLICANT: West, Brian L.
APPLICANT: Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
                                                                                                                                                                                                                                                                                        US-08-980-115-9
; Sequence 9, Applicati
; Patent No. 6266622
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                        APPLICANT: Scanlan, Thomas S. APPLICANT: Baxter, John D. APPLICANT: Fletterick, Robert J. APPLICANT: Wagner, Richard L. APPLICANT: Kushner, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
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INFORMATION FOR SEQ ID NO:
EARLIER APPLICATION NUMBER: 60/008,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura Toni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Local Similarity 63.8%;
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Pred. No. 9.8
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; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-9
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08459287
Patent No. 5686596
GENERAL INFORMATION:
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EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTMARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mukherjee, Ranjan
TITLE OF INVENTION: HUMAN PEROXISOME PROLIFERATOR ACTIVATED
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                           STREET: 611 West S:
CITY: Los Angeles
STATE: California
COUNTRY: USA
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                                                    APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER:
                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVI 357
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611 West Sixth Street
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                                                                    US/08/459,287
08/143,215
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RESULT 13
US-08-484-200-4
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                                                                                                                                                           Sequence 4, Application US/08484200 Patent No. 5861274
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                                                                           GENERAL INFORMATION:
APPLICANT: EVANS,
APPLICANT: FORMAN, BARRY M.
APPLICANT: KLIEWER, STEVEN,
APPLICANT: ONG, ESTELITA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: October 25, 1993
APPLICATION NUMBER: 08/141,500
FILING DATE: October 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
               NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                       REFIKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDI 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMT
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                                                                                                                                                                                                                                                                                                                                                     QDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLL 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHLYDSYIKSFPLT 195
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                                                                              KLIEWER, STEVEN A. ONG, ESTELITA S.
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PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
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                                              NOVEL MEMBERS OF THE STEROID/THYROID SUPERFAMILY AND USES THEREFOR
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Pred. No. 5.9
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.9e-86;
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US-08-459-287-2
; Sequence 2, Application US/08459287
; Retent No. 5586596
; GENERAL INFORMATION:
; APPLICANT: Mukherjee, Ranjan
; TITLE OF INVENTION: HUMAN PEROXIS
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 3
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Best Local Similarity 62.3
Matches 203; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 KTQLYNRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADL 177
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STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 07-JUN
                                CITY: Los Angeles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                STREET:
                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLA
                                                                                                                                                                                                                                                                                                                                                                                                  ILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQ 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPYNEISVHVFYRCQSTTVETVRELTEFAKNIPNFSSLFLNDQVTLLKYGVHEAIFAMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAFSKHIYNAYLKNFNMTKKKARSILTGKSSHNAPFVIHDIETLWQAEKGLVWKQLVNGL 234
                                                                                                                                                                                                                                                                                                                                                                 ILCGDRPGLMNVPQVEAIQDTILRALEFHLQVNHPDSQYLFPKLLQKMADLRQLVTEHAQ
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                California
                                              E: Lyon & Lyon
611 West Sixth Street
                                                                                                                              Mukherjee, Ranjan
NVENTION: HUMAN PEROXISOME PROLIFERATOR ACTIVATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.7%; Score 1076.5; DB 2; Length 62.3%; Pred. No. 1.5e-85; tive 58; Mismatches 64; Indels
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AFR: P41
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 antino acids
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/143,215
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 415
                  390 NHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: October 25, 19 APPLICATION NUMBER: 08/141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                       MEPKFEFAVKFNALELDDSDLAIFTAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKL 389
                                                                                                                                                      PGEVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDF 329
                                                                                                                                                                                                                                                                              NHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKTESDAALHPLLQEIYRDMY 468
                                                                    MEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIEKMQEGIVHVLRLHLQS
                                                                                                                                    PGFANLDLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNGFITREFLKSLRKPFCDI 354
                                                                                                                                                                                                           NPPFVIHDMETLCMAEKTLVAK-LVANGIQNKEAEVRIFHCCQCTSVETVTELTEFAKAI 294
                                                                                                                                                                                                                                             KSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSI 269
                                                                                                                                                                                                                                                                                                                                                   VHACEGCKGFFRRTIRLKLVYDKCDRSCKIQKKNRNKCQYCRFHKCLSVGMSHNAIRFGR
                                                                                                                                                                                                                                                                                                                                                                                                                        PGSDGSVITDTLSPASSPSSVTYPVVPG-----SVDESPSGALNIECRICGDKASGYHYG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DFSSIS-TPHYEDIPFTRTDPVVADYKYDLKLQEYQS-AIKVE-----PASPPYY- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVDTESPLCPLSPLEAGDLESPLSEEFLQEMGNIQEISQSIGEDSSGSFGFTEYQYLGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 22, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.7%;
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Pred. No. 1.66
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RESULT 15
US-08-764-870-8
; Sequence 8, Application US/08764870
; Patent No. 6236946
; GENERAL INFORMATION:

APPLICANT:

Thomas

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: UCL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: West, Brian
TITLE OF INVENTION: Nuclear Receptor
TITLE OF INVENTION: Binding Domains
                     210 KSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSI 269
236 NPPFVIHDMETLCMAEKTLVAK-LVANGIQNKEVEVRIFHCCQCTSVETVTELTEFAKAI
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                                                                                                                                   116 VHACEGCKGFFRRTIRLKLVYDKCDRSCKIQKKNRNKCQYCRFHKCLSVGMSHNAIRFGR
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CITY: P
STATE:
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                                                                                                                                                                                                     61 PGSDGSVITDTLSPASSPSSVTYPVVPG----SVDESPSGALNIECRICGDKASGYHYG 115
                                                                                                                                                                                                                                                                                                     NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                               ---DFSSIS-TPHYEDIPFTRTDPVVADYKYDLKLQEYQS-AIKVE-----PASPPYY- 116
                                                                                                                                                                                                                                                                      MVDTESPLCPLSPLEAGDLESPLSEEFLQEMGNIQEISQSIGEDSSGSFGFTEYQYLGSC 60
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Fletterick, Robert J
Wagner, Richard L
Kushner, Peter J
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Five Palo Alto Square,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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49.8%;
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                                                             MEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKL 389
NHPDDIFLFPKLLQKMADLRQLVTEHAQLVQTIKKTESDAALHPLLQEIYRDMY 468
                                                 MEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIEKMQEGIVHVLRLHLQS
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Search completed: February 25, Job time : 30 secs 2003, 04:02:38



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Command line parameters:

-MODEL-framet_p2n.model -DEV=xlh
-O-/Cgn2_1/USPTO_Spool/US09931007/runat_14022003_102554_4697/app_query.fasta_1.839
-OB-ISSUED_PATENTS_NA -OFMT-fastap -SUFFIX=p2n.rni -MINNATCH+0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US09931007_eGGN_1_1_32 erunat_14022003_102554_4697 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=10 -XGAPOP=6 -FGAPEXT=7
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Maximum DB
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score greater than or equal to the score of the result being printed,
   Score
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
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US-09-514-247N-5

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US-08-134-557D-1

US-08-285-392-1

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US-08-477-493-1

US-08-484-200-3
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US-08-372-652-7	S91-00399-	-336-4	96-6	4-1288	US-08-342-411A-3	S95-16311-	-652-1	-07266	σ	7-737-736	-592-383	-694-501-	8-463	-333-358	2-	-US92-02320A	-08-095-728B-	08-306-691B-	167	.1	PCT-US92-02320A-3	-80-	S-08-1	9	-08-917-653-	501	-08-463-694-	33-358-	US-08-917-653-3	8-459-287-	S-08-694-501-	US-08-463-694-9
Sequence 7, Appli	e 5,	5	e 1,	e 4,	e ω,	e 14,	14,	<u>, , , , , , , , , , , , , , , , , , , </u>	<u>, , , , , , , , , , , , , , , , , , , </u>	6	Sequence 3, Appli	7,	Sequence 7, Appli	7	. 526043	۳	1, Appl	equence 52, App	Patent No. 5171671	1,	ω	equence 3, A	equence 13, App	Patent No. 5223606	equence 4,	equence 1,	equence 1,	e 1,	e 3,	O	e 9,	Sequence 9, Appli

## ALIGNMENTS

RESULT 1 US-09-128-142-3

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Sequence 3, Application.

Sequence 3, Application.

Sequence 3, Application.

Patent No. 6394559

; GENERAL INFORMATION:
   APPLICANT: Smith, Roy G.

APPLICANT: Smith, Roy G.

TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH

PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMAL AND
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: Power Macintosh 7500/100
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                               APPLICATION NUMBER: 08/844,007 FILING DATE: <Unknown> ATTORNEY_AGENT INFORMATION:
                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                    NAME: Tribble, Jack L. REGISTRATION NUMBER: 32,633
                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/128,142 FILING DATE: 03-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 126
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
                    TELEFAX:
                                      TELEPHONE: (908) 594-5321
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07065-0907
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                      (908)
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1518 base pairs
; TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID N
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Best Local Similarity:
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                                                               GlnLeuTyrAsn-----
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                                                                                                           ValGlyMetSerHisAsnAlaIleArgPheGlyArgMetProGlnAlaGluLysGluLys 158
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LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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87.72%
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APPLICANT: Robert McKay
APPLICANT: Alexander H. Borchers
APPLICANT: Brenda F. Baker
TITLE OF INVENTION: ANTISENSE MODULATION OF PER
FILE REFERENCE: RTS-0104
CURRENT APPLICATION NUMBER: US/09/484,345
CURRENT FILING DATE: 2000-01-18
; NAME/KEY: CDS
; LOCATION: (91)...
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                               FEATURE:
                                        TYPE: DNA ORGANISM: Homo
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Alignment Scores

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es: city: llarity:	IT NO. 6365361 IT NO. 6365361 ALL INFORMATION: JICANT: TANABE SEIYAKU CO. LTD. JICANT: TANABE SEIYAKU CO. LTD. JICANT: TANABE SEIYAKU CO. LTD. JICANT: TANAGUCHI, TOMOYASU JICANT: TANIGUCHI, TOMOYASU JICANT: MIZUKAMI, JUNKO JE OF INVENTION: METHOD FOR IDENT REFERENCE: TANIGUCHI-6 REFILING DATE: 2000-02-28 REFILING DATE: 2000-02-8 REFILING DATE: 1998-08-24 NR APPLICATION NUMBER: JPZ31084/1 REFILING DATE: 1997-08-27 DR APPLICATION NUMBER: JPZ31084/1 NR FILING DATE: 1997-08-27 SER OF SEQ ID NOS: 10 UNOS: 10 UNOS: 10 UNOS: 10 UNOS: 1679 EE: DAA ANISM: Homo sapiens VIURE: IE/KEY: CDS ATION: (159)(1679)	TACAAGGACTTGTAC	sAspLe	nValIl         GTGAT	SLeuLe        CTGCT	JG1nA1.	rGlyAs         GGAGA	eAsnAl         CAATGC	SSerLe       SAGCCT	CASnLy        GAATAA	1ValTh        1GTAAC	nGluIl         GAGAT
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Length: Matches: Conservati Mismatches Indels:	247A .TD. IDENTIFYING 709/514,247A 18 1998/03734 084/1997			spMets         ACATGP	euArgo          TCAGAC	ysLeu <i>l</i>         AGCTG <i>l</i>	SnValI        ATGTGP	erAspI        GCGACT	SpPhek         ACTTT#	erGluc         CCGAGG	alHise	erIler        GCATTO
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                          TELEFAX: (908)
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Smith,
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                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: Power Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/128,142
FILING DATE: 03-Aug-1998
CLASSIFICATION: <Unknown>
                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
                                                                                                                          APPLICATION NUMBER: 08/844,007
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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CITY: Rahway
STATE: New Jersey
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                                                                                                REGISTRATION NUMBER:
                                                                                                               NAME: Tribble, Jack L.
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                             ID NO:
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TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO

US-09-128-142-1
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Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
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                             SerTyrIleLysSerPheProLeuThrLysAlaLysAlaArgAlaIleLeuThrGlyLys
                                                                                                                                                  AspLeuSerValMetGluAspHisSerHisSerPheAspIleLysProPheThrThrVal
ArgPheGlyArgMetProGlnAlaGluLysGluLysLeuLeuAlaGluIleSerSerAsp
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STATE: IL COUNTRY: USA ZIP: 60601  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALID OPERATING SYSTEM: PC-DOS/ SOFTWARE: PATENTIA Releas CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Katz, Martin L. REGISTRATION NUMBER: 25,0 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATIO TELEPHONE: 312-616-5400 TELEFAX: 312-616-5460	SULT 5 -08-134-557D-1 -08-134-557D-1 Sequence 1, App Patent No. 6200 GENERAL INFORM APPLICANT: 1 APPLICANT: 1 TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TOMBER OF SEE CORRESPONDEN ADDRESSEE: 2 STREET: 2 CITY: Chi-	427 ThrAspMe 	407 A	1201 C	347 A 1141 G 367 L	327 GlyAspPhe          1081 GGTGACTTT	307 IleSerG]          1021 ATATCCG/	287 GLyValHis         961 GGAGTCCAC	267 LysSerIleP:	247 IL    841 AT
TTE: IL  NTRY: USA  : 60601  TER READABLE FORM:  IUM TYPE: Floppy disk  PUTER: IBM PC compatible  RATING SYSTEM: PC-DOS/MS-DOS  RATING SYSTEM: PC-DOS/MS-DOS  TARAE: PatentIn Release #1.0, Version #1.30  NT APPLICATION DATA:  LICATION UMBER: US/08/134,557D  ING DATE:  ING DATE:  ING DATE:  SSIFICATION: 435  SSIFICATION UMBER: US/08/134,557D  ING DATE:  E: Katz, Martin L.  E: Katz, Martin L.  E: Katz, Martin L.  E: Katz, Martin L.  GRENGE/DOCKET NUMBER: ARCH:098  OMMUNICATION INFORMATION:  EPHONE: 312-616-5460  EFAX: 312-616-5460	lication US/08134557D 802 RATION: Sizeene, Marianne E. Blumberg, Bruce BLUmberg, Human Peroxisome Proliferator Activated ENTION: Receptor Gamma: Compositions and Methods DUENCES: B. DE ADDRESS: Rockey, Milnamow & Katz, Ltd. Prudential Plaza, Suite 4700 180 N. Stetson cago	SerLeuHisProLeuLeuGlnGluIleTyrLysAspLeuTyr 443	alGlnLeuLeuGlnValIleLysLysThrGlu 		To To	MetGluProLysPheGluPheAlaValLysPheAsnAlaLeuGluLeuAsp 	uglyglnglyphemetthrargglupheLeuLysSerLeuargLysProphe 	GluIleIleTyrThrMetLeuAlaSerLeuMetAsnLysAspGlyValLeu 	roGlyPheValAsnLeuAspLeuAsnAspGlnValThrLeuLeuLysTyr 	ePheGlnGlyCysGlnPheArgSerValGluAlaValGlnGluIleThrGluTyrAla 
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SEQUENCE CHARACTERISTICS:
LENGTH: 1844 base pair
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MOLECULE TYPE:
FEATURE:
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STRANDEDNESS: single
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AlaGluIleSerSerAspIleAspGlnLeuAsnProGluSerAlaAspLeuArg---Ala
                                                                                                                           MetSerHisAsnalaIleArgPheGlyArgMetProGlnAlaGluLysGluLysLeuLeu
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                                                                          GCGGAGATCTCCAGTGATATCGACCAGCTGAATCCAGAGTCCGCTGACCTCCGTCAGGCC
                                                                                                                CACAAAAAAAGTAGAAATAAATGTCAGTACTGTCGGTTTCAGAAATGCCTTGCAGTGGGG
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                                                                                                                                                                                        Sequence 1, Application Patent No. 6214850 GENERAL INFORMATION:
        ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
                                                                                                                 APPLICANT: Evans, Ronald
APPLICANT: Forman, Barry
TITLE OF INVENTION: MODI
TITLE OF INVENTION: ACT:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: PIETLY, Sci
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CITY: Los Angeles
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COUNTRY: USA
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                                                                                                           444 South
                                                                                                                                    FORMAR, RONALD M.

FORMAR, BAIRY M.

VENTION: MODULATORS OF PEROXISOME PROLIFERATOR VENTION: ACTIVATED RECEPTOR-GAMMA, AND METHODS SQUENCES:
                                                                                                            Flower Street,
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                                                                                                           Schroeder, Brueggemann &
Flower Street, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEPAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                AATAAATGTCAGTACTGTCGGTTTCAGAAGTGCCTTGCTGTGGGGATGTCTCACAATGCC
                                                           AsnLysCysGlnTyrCysArgPheGlnLysCysLeuAlaValGlyMetSerHisAsnAla 145
                                                                                             CGATTGAAGCTTATTTATGATAGGTGTGATCTTAACTGCCGGATCCACAAAAAAAGTAGA
                                                                                                                                         GGCTTCCACTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTTTTCCGAAGAACCATC 762
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TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 base pairs
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REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
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ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,200
FILING DATE: 07-JUN-1995
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MEDIUM TYPE: Floppy disk
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LOCATION:
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COUNTRY:
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                                                    GGCTTCCACTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTTTTCCGAAGAACCATC 762
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Matches:
Conservative:
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0	Qy 126	CysGlnTyrCysArgPheGlnLysCysLeuAlaValGlyMetSerHisAs
п	82	
0	Qy 146	lnAlaGluLysGluLysLeuLeuAlaGluIleSe
п	88	
0	Оу 166	6 AsplieAspGinLeuAsnProGluSerAlaAspLeuArgAlaLeuAlaLysHisLeuTyr 185
п	Db 94:	3 GATATCGACCAGCTGAACCCAGAGTCTGCTGATCTGCGAGCCCTGGCAAAGCATTTGTAT 1002
n	Qу 186	spSerTyrIleLysSerPheProLeuThrLysAlaLysAlaArgAlaIleLeuThrC
	Db 1003	3 GACTCATACATAAAGTCCTTCCCGCTGACCAAAGCCAAGGCGAGGGCGATCTTGACAGGA 1062
Ω.	Оу 206	6 LysThrThrAspLysSerProPheValIleTyrAspMetAsnSerLeuMetMetGlyGlu 225
ь	Db 1063	3 AAGACAACGGACAAATCACCATTTGTCATCTACGACATGAATTCCTTAATGATGGGGAGAA 1122
0	Qy 226	LysIleLysPheLysHisIleThrProLeuGlnGluGlnSerLysGluValA]
ь	Db 112:	AAATCAAG
0	Оу 246	6 ArgilePheGlnGlyCysGlnPheArgSerValGluAlaValGlnGluIleThrGluTyr 265
	Db 1183	3 CGAATTTTTCAAGGGTGCCAGTTTCGATCCGTAGAAGCCGTGCAAGAGATCACAGAGTAT 1242
n	Оу 266	6 AlaLysSerIleProGlyPheValAsnLeuAspLeuAsnAspGlnValThrLeuLeuLys 285
В	Db 1243	GCCAAAAATATCCCTGGTTTCATTAACCTTGATTTGAATGACCAAGTGACTCTGCTC
γQ	у 286	6 TyrGlyValHisGluIleIleTyrThrMetLeuAlaSerLeuMetAsnLysAspGlyVal 305
п	Db 1303	TATGGTGTCCATGAGATCATCTACACGATGCTGGCCTCCCTGATGAATAAAGATGGAGT
Qy	ω	6 LeuIleSerGluGlyGlnGlyPheMetThrArgGluPheLeuLysSerLeuArgLysPro 325
Db		CTCATCTCAGAGGGCCAAGGATTCATGACCAGGGAGTTCCTCAAAAGCCTGCGGAA
Qy	ω	6 PheGlyAspPheMetGluProLysPheGluPheAlaValLysPheAsnAlaLeuGluLeu 345
ДD	ь 1423	TTTGGTGACTTTATGGAGCCTAAGTTTGAGTTTGCTGTGAAGTTCAATGCACTGGA
γ <del>γ</del>	Qy 346 nh 1483	6 AspAspSerAspLeuAlaIlePheIleAlaValIleIleLeuSerGlyAspArgProGly 365 
Qy		LeuLeuAsnValLysProIleGluAspIleGlnAspAsnLeuLeuGlnAlaLeuGluLeu 385
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δĀ	у 386	GlnLeuLysLeuAsnHisProGluSerSerGlnLeuPheAlaLysLeuLeuGlnLys
ДQ	b 1603	CAGCTCAAGCTGAATCACCCAGAGTCCTCTCAGCTGTTCGCCAAGGTGCTCCAGAAGAT
νo	у 406	Thra
Db	b 1663	ACAGACCTCAGGCAGATCGTCACAGAGCACGTGCAGCTACTGCATGTGATCAAGAAGAC
Qy		6 GluThrAspMetSerLeuHisProLeuLeuGlnGluIleTyrLysAspLeuTyr 443
Db	b 1723	GAGACAGACATGAGCCTTCACCCCCTGCTCCAGGAGATCTACAAGGACTT
🗆 🗷	ESULT 8 IS-08-477 Sequenc	T 8 -477-493-1 uence 1, Application US/08477493 ent No. 5939442
., ., .	GE	NT: Evans, Ronald M
	APPI TITI	LICANT: FORMAN, BARRY M.  LE OF INVENTION: MODULATIONS OF PEROXISOME PROLIFERATOR  FOR INVENTION: MODULATIONS OF PEROXISOME PROLIFERATOR
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TITLE OF INVENTION: ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF

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; LOCATION:
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DB:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 1:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,493
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
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NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroe
STREET: 444 South Flower
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STREET: 444 South I
CITY: Los Angeles
STATE: CA
COUNTRY: USA
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                                                                                    ProValValAlaAspTyrLysTyrAspLeuLysLeuGlnGluTyrGlnSerAlaIleLys
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                        LeuLeuAsnValLysProIleGluAspIleGlnAspAsnLeuLeuGlnAlaLeuGluLeu
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Sequence 1, Application Patent No. 6022897

US/08465375A

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GENERAL INFORMATION:
APPLICANT: EVANS, RONALD M.
APPLICANT: EVANS, RONALD M.
APPLICANT: EVANS, RONALD M.
TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: SALK1470-1
CURRENT APPLICATION NUMBER: US/08/465,375A
CURRENT FILING DATE: 1995-06-05
EARLLER APPLICATION NUMBER: 08/428,559
EARLLER APPLICATION NUMBER: 08/48,559
EARLLER APPLICATION NUMBER: 08/48,559
EARLLER FILING DATE: 1995-04-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2005
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Sequence 1, Application US/09788070; Patent No. 6413994; GENERAL INFORMATION: APPLICANT: EVANS, RONALD APPLICANT: FORMAN, Barry TITLE OF INVENTION: MODULATORS OF PETITLE OF INVENTION: AND METHODS FOR FILE REFERENCE: SALK1480-2
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn vers
SEQ ID NO 1
LENGTH: 2005
                                             CURRENT APPLICATION NUMBER: US/09/788,070 CURRENT FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: US 09/955,302 PRIOR FILING DATE: 1999-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application Patent No. 5861274
                                                                                                                CORRESPONDENCE ADDRESS:

ADDRESSE: PRETTY, SCHROEDER, BRUEG
STREET: 444 SOUTH FLOWER STREET, SU
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                     APPLICATION NUMBER: US/08/484,200 FILING DATE: 07-JUN-1995 CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               APPLICANT: EVANS, RONALD M.
APPLICANT: FORMAN, BARRY M.
APPLICANT: KLIEMER, STEVEN A.
APPLICANT: ONG, ESTELITA S.
TITLE OF INVENTION: NOVEL MEMBERS OF THE STEROID/THYROID
TITLE OF INVENTION: SUPERFAMILY AND USES THEREFOR
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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            NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
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              9971
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                                                                                                                                   Version
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TELEFAX:

TELEPHONE:

619-546-1995 619-546-9392

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Best Local Similarity:
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STRANDEDNESS: both
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                                                                                      SerLeuMetAsnLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGlu 317
                                                                                                                                                                                                                           AsnAspGlnValThrLeuLeuLysTyrGlyValHisGluIleIleTyrThrMetLeuAla
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IleLeuSerGlyAspArgProGlyLeuLeuAsnValLysProIleGluAspIleGlnAsp 377
                                                                                                                                                                                                           AATGACCAGGTGACCCTCCTCAAGTATGGCGTGCACGAGGCCATCTTTGCCATGCTGGCC
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US-08-333-358-9
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                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Relier Ph.D., Stephen E.
REGISTRATION UNUBER: 31192
REFERENCE/DOCKET NUMBER: P31 893
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHAX: (619) 535-9049
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 90071-3921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                           IMMEDIATE CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1505
                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: YAO MI., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 444 SO. F
CITY: Los Angeles
STATE: CA
                             NAME/KEY:
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                                                                                                                                   nucleic acid
                                                             XR4
                                                                             SOURCE:
                                                                                                                                                     2009 base pairs
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ORO Ph.D., ANTHONY E.
BORGMEYER Ph.D., UWE K.
GIGUERE Ph.D., VINCENT NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVANS Ph.D., RONALI MANGELSDORF Ph.D.,
                                                           (XR4.SEG)
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                               LeuLeuGlnValIleLysLysThrGluThrAspMetSerLeuHisProLeuLeuGlnGlu
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|AAGGCCCGGAGCATCCTCACCGGCAAGTCCAGCCACCACGACCCTTTGTCATCCACGAC
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Best Local Similarity:
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                                                          US-09-931-007A-1 (1-688) x US-08-463-694-9 (1-2009)
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5696233
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FILING DATE: 17-SEP-1991
ATTORNEY_AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: 931 893
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                     FEATURE:
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LENGTH: 2009 base pair
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COMPUTER READABLE FORM:
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APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO MI., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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LOCATION:
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COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
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SYSTEM: PC-DOS/MS-DOS
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                                                                           Sequence 9, Applic Patent No. 5710004
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
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                                                                                         Application US/08694501
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-694-501-9
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Reiter Ph.D., Stephen REGISTION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US/07/761,068
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                ArgAlaLeuAlaLysHisLeuTyrAspSerTyrIleLysSerPheProLeuThrLysAla :::||| :::||| :::|||
                                                        CTCGGCATGTCGCACAACGCTATCCGCTTTGGACGGATGCCGGACGGCGAGAAGAGGAAG
                                                                                                                                      ValGlyMetSerHisAsnAlaIleArgPheGlyArgMetProGlnAlaGluLysGluLys 158
                                                                                                                                                                                   AAGATCCAGAAGAAGAACCGCAACAAGTGTCAGTACTGCCGCTTCCAGAAGTGCCTGGCA
                                                                                                                                                                                                LysThrGlnLeuTyrAsnArgAsnLysCysGlnTyrCysArgPheGlnLysCysLeuAla 138
AAGGCCTTCTCTAAGCACATCTACAACGCCTACCTGAAAAACTTCAACATGACCAAAAAG
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                                                                                                                                                                                                              GENERAL INFORMATION:
                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM compatible
                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                            APPLICANT: Mukherjee,
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 OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                          CITY: Los Angeles
STATE: California
                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1407 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: October 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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151 MetProGlnAlaGluLysGluLysLeuLeuAlaGluIle---
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FILING DATE: October 25, 1993
APPLICATION NUMBER: 08/141,500
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 MetValAspThrGluMetProPheTrpProThrAsn-------
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                                                                                                                                                                                                                                                                                                   GTGACTTATCCTGTGGTCCCCGGC--
                                                                    CysArgPheGlnLysCysLeuAlaValGlyMetSerHisAsnAlaIleArgPheGlyArg 150
                                                                                                                                                                                                                                     GGAGCATTGAACATCGAATGTAGAATCTGCGGGGACAAGGCCTCAGGCTATCATTACGGA
                                                                                                                                                                                                                                                                                                                                                                 CCTGGCTCAGATGGCTCGGTCATCACGGACACGCTTTCACCAGCTTCGAGCCCCTCCTCG
                                                                                                             TATGACAAGTGCGACCGCAGCTGCAAGATCCAGAAAAAGAACAGTTTCAAATGCCAGTAT
                                                                                                                                                                                                                                                                     ---AlaIleLysValGlu------ProAlaSerProProTyrTyr---
                                                                                                                                                                                                                                                                                                                              ArgThrAspProValValAlaAspTyrLysTyrAspLeuLysLeuGlnGluTyrGlnSer 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValMetGluAspHisSerHisSerPheAspIleLysProPheThrThrVal------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGTGGACACGGAAAGCCCACTCTGCCCCCTCTCCCCACTCGAGGCCGGCGATCTAGAG
                                                 -----AspPheSerSerIleSer---ThrProHisTyrGluAspIleProPheThr 84
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AsnHisProGluSerSerGlnLeuPheAlaLysLeuLeuGlnLysMetThrAspLeuArg 409
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                                                                                                                             LeuAlaIlePheIleAlaValIleIleLeuSerGlyAspArgProGlyLeuLeuAsnVal 369
                                                                                                                                                                                                                                                                                                             AATCCACCTTTTGTCATACATGATATGGAGACACTGTGTATGGCTGAGAAGACGCTGGTG
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Search completed: February 25, 2003, 04:10:34 Job time: 87 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8 2106.5 60.0 811 22 AAB85801 Human 9 2106.5 60.0 874 22 AAB85795 Human	60.0 811 22 AAB85801 60.0 874 22 AAB85795	60.0 811 22 AAB85801	60.0 811 22 AAB85801	60.0 811 22 AAB85801	60.0 811 22 AAB85801	60.0 811 22 AAB85801	60.0 811 22 AAB85801	60.0 811 22 AAB85801	60.0 811 22 AAB85801	50 0 ST 33 NOSSBOT		֡	COLOR ENTITIONS	TA TO TO A PROPERTY OF THE PRO		100 11 1100000	SUCCESSION AND AND AND AND AND AND AND AND AND AN	63 6 EOE OO NATOEOOO		CU.O JOU AS PARTISONO	7 7 7 7 7 NOTE 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	01.0 (0) F. MINULIO	DA D JOJ - ABECCASS	CO C C 13 ****COSCC	41.10	h/ Cl 4h/ C/ ARR/huss		TOTAL BUILDINGS	9X X 750 73 ABB09779	00.0 /UV 44 ADD/030/	09 8 750 00 Nat 76007		. מכסות שמיכוז הפוזלרוו הם דה	Watch I canth Da In	COURT KUCTY	Pagil t Olipry	•
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Composition providing inducible expression of a nucleic acid, useful in gene therapy, uses minimal promoter with peroxisome proliferator-activated receptor response elements -

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AAR33/45 AAB53489 AAR51555 AAR71565 ABB63705 AAR13791 AAR81894 AAR33741	AAY05472 AAR92479 AAR99597 AAR74053 AAR20342 AAY21633 AAY25470	AAR92478 AAW9596 AAB67656 AAY21635 AAG74068 AAY21634 AAR41875 AAR89214	AAR99323 AAB85794 AAR99324 AAR99327 AAE12867 AAR99325 AAR99328 AAR99328 AAR99328 AAR99328 AAR98802 AAB85802 AAB85802 AAB85802 AAB85802
XR4. Mus musculus Human colon cancer Human colon cancer EAR-1r gene produc Drosophila melanog E75A protein. Dro Bovine PPAR. Bos XR1. Homo sapiens	n PPAR delta xisome prolif e peroxisome n peroxisome rxisome prolif nd binding do n PPAR alpha	Peroxisome prolite Mouse peroxisome p Human peroxisome p Ligand binding dom Human colon cancer Ligand binding dom Steroid hormone re Peroxisome prolife	Peroxisome prolife Human PAX8e8-PPARg Peroxisome prolife Peroxisome prolife Peroxisome prolife Human peroxisome prolife Peroxisome prolife Peroxisome prolife Human PPAR-gamma pr Human PPAR-gamma pr Human peroxisome p Human peroxisome p

## ALIGNMENTS

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RESULT 1
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IID ABB76987
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XX ABB76987
XX Huma
XX Huma
XX PPAR
KW PPAR
KW PPAR
KW PEO
OS Homo
OS Homo
OS Homo
XX W22-J
XX 28-D
PR 22-J
PF 22-J
PR 20-A
XX AX
PR 22-J
PR 20-A
XX AX
PR 22-J
PR 20-A
XX AX
PR 20-A
XX Comp
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20-AUG-1999;
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99US-0149721.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that consists of a PPAR (peroxisome proliferator-activated receptor) response element (ABL58055) and a minimal promoter; and/or a component (A2) comprising a nucleic acid encoding a PPAR under control of a transcriptional promoter: (A), and vectors containing (A1) and (A2), are used to express (I) in cells for expression of transgenic (I) for experimental, clinical, therapeutic or diagnostic purposes. (I) encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an agriculturally useful, therapeutic, vaccinating or marker protein and is most especially expressed in human muscle cells. Cells containing (A), or the vectors, are used to identify PPAR ligands or to produce transgenic animals for preclinical studies, analysis of bioavailability, transgenic animals for preclinical studies, analysis of bioavailability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                     TMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIF
                                                                                                                                                                                                                               EHVQLLQVIKKTETDMSLHPLLQEIYKDLY 688
                                                                    IAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVT
                                                                                                                                                              TMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIF
                                                                                                                                                                                                                                                                                                                              LQVIKKTETDMSLHPLLQEIYKDLYAWAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHI
                                                                                                                                                                                                                                                                                                                                                    LQVIKKTETDMSLHPLLQEIYKDLYAWAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHI 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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91.7%;
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Pred. No. 1
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1.2e-264;
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                                                                                                  cc introducing, into a non-human animal tissue or target cell a nucleic caid comprising the transgene and encoding a transcript (T1); and cc a nucleic acid that encodes a transcript (T2) that inhibits T1
cc specifically. Both nucleic acids are co-expressed so that activity of CT is inhibited constitutively by T2. The nucleic acids are controlled by a transcriptional promoter and the activity of T2 and/or T1 can be regulated by an external agent. The method is used to regulate a cut transgene, in animals and plants, particularly for control of therapeutic cut transgenes in treatment of genetic anomalies and defects, e.g. cut transgenes in treatment of genetic anomalies and defects, e.g. cut casses, hormonal disorders, haemophilia, inflammation (rheumatoid colorarthritis), beta-thalassemia, cancer (by inducing apoptosis or expression of toxins), neurodegeneration, cardiovascular diseases (hypertension), hyperlipidaemia (obesity), and in preparation of coxaccines. Transgenic animals containing T1 and T2 are useful as experimental models of diseases and transgenic plants are useful for studying the effects of specific genes on development etc.
 Matches
                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                             receptor (PPAR)alpha. This receptor may be used to regulate expression of a transgene. The specification describes a method for regulating expression of a selected transgene in vivo. The method comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgene; mitochondrial disease; myopathy; ischaemia; stenosis; lysosomal storage disease; hormonal disorder; haemophilia; inflammation; rheumatoid polyarthritis; beta-thalassemia; cancer; neurodegeneration; cardiovascular disease; hypertension; hyperlipidaemia; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents human peroxidome preceptor (PPAR)alpha. This receptor may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulating for gene the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 15; 123pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence that expresses an inhibitory transcript
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                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ng expression of transgenes in plants and animals; useful e.g.
therapy, comprises cotransfection with a transgene and a
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                                                                                                                                                                                       PPAR response element; PPAR; vaccine;
                                                                                                                                                                                                                          Human PPARgamma2gamma2 E/F domain.
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                     22-JUN-2000; 2000WO-FR01744
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transcriptional promoter. (A), and vectors containing (A1) and (A2), are used to express (I) in cells for expression of transgenic (I) for expression of transgenic (I) for experimental, clinical, therapeutic or diagnostic purposes. (I) encodes an agriculturally useful, therapeutic, vaccinating or marker protein and is most especially expressed in human muscle cells. Cells containing (A), or the vectors, are used to identify PPAR Ilgands or to produce transgenic animals for preclinical studies, analysis of bioavailability, labelling etc. The present sequence is the E/F domain of human PPARgamma2gamma2, which was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a composition (A) comprising a compone (A1) containing a nucleic acid (I) controlled by an inducible promoter that consists of a PPAR (peroxisome proliferator-activated receptor) response element (ABL58055) and a minimal promoter; and/or a component (A2) comprising a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a PPAR under control of a proposition of a nucleic acid encoding a ppart and a nucleic acid encoding a nucleic acid 
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30-JAN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cycle enzymes. Peroxisome proliferators include unsaturated fatty acids, hypolipidemic drugs, and herbicides. PPARgamma has two main subtypes (hPPARgamma, and hPPARgamma), which differ in their N-terminal sequences, and are expressed at high levels in adipose tissue. HPPARgamma proteins repress hPPARalpha activity. These proteins can be used in a cell system with a reporter gene (and optionally a hPPARalpha protein) to identify agonists and antagonists of the polypeptides, which can be used as therapeutic agents. The agonists and antagonists can be used to treat obesity, diabetes, anorexia, hyperlipidaemia, hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences differ in their N-Lermina, sequences, and respiration enzymes for cholesterol and lipid metabolism, and respiration enzymes to recovisome proliferators increase the capacity of the peroxisomes to metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression of the beta-oxidation metabolise fatty acids, via increased expression acids                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human peroxisome proliferator activated receptor(s), hPPAR-gamma and hPPAR-gamma2 - useful to identify polypeptide (ant)agonists to treat e.g. obesity, anorexia and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR99326-R99328 represent the three different subtypes of human peroxisome proliferator activated receptor gamma2 (hPPARgamma2) sequences differ in their N-terminal sequences. Peroxisomes con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pattern for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypercholesterolaemia, hyperlipoproteinaemia, and other metabolic disorders. These sequences, the DNA encoding them, and antibodies against them, can be used to establish a tissue specific expression
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herbicide; hPPARgamma2; adipose tissue; obesity; diabetes; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peroxisome proliferator activated receptor gamma; PPAN peroxisome; cholesterol metabolism; lipid metabolism;
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                                                                   DIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKT
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95US-0484487.
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No. 1.9e-167;
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                                       The invention is useful for treating cancer and other disorders including excessive cell proliferation and viral infection. The invention is also directed to the use of PPAR gammal and gamma2 to identify compounds that are antiproliferative, antiviral and antitumour agents. The invention
composition comprising thiazolidinedione in an amount modulate PPAR gammal and gamma2 activity. The present
                             also relates to a method of treating cancer using a pharmaceutical
                                                                                                                                                                                                                                                                                                                 02-MAY-1996;
18-APR-1997;
                                                                                                                                                                               Use of thiazolidinedione for treating
                                                                                                                                                                                                             N-PSDB; AAD21022
                                                                                                                                                                                                                           WPI; 2001-647265/74
                                                                                                                                                                                                                                                                                                                                                            03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytotoxic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peroxisome proliferator activated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE12868 standard;
                                                                                                                      The invention relates to compounds and ligands that bind to human
                                                                                                                                                   Example
                                                                                                                                                                                                                                                        Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                     peroxisome proliferator
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                                                                                                                                                 3; Fig 4; 17pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                      פט
                                                                                                                                                                                                                                                                                                                96US-016694P
97US-0844007
                                                                                                                                                                                                                                                                                                                                                            98US-0128142
                                                                                                                                                                                                                                                                                      CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e proliferator activated receptor gamma2; roliferative; antiviral; cancer; cell pro pharmaceutical; thiazolidinedione.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                     activated receptors (PPAR) gammal and gamma2
                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505
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                                                                                                                                                                                and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PPAR) gamma2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation;
                                                                                      including
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Best Local
                                                    (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                   20-JAN-2000;
14-AUG-2000;
                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                                                                                            WO200152789-A2
                                                                                                                                                                                                                                                                                                                                                                                                       PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PPARgamma protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB85800
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                                                                                                                                                                              18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                  tollicular carcinoma;
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443; Conser
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                                                                                                   2000US-0177109.
2000US-0225079.
                                                                                                                                                                              2001WO-US01664
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Pred. No. 1.9e-167;
0; Mismatches 0;
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Best Local
                          Human PPARgamma
                                                                                                                 AAB59839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subject having a disorder characterized by the presence of a PAX8-PPARGammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARGammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a
                                                        27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oncogene designated PAX8-PPARgammal that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR
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                                                                                                                                                                                                   LQVIKKTETDMSLHPLLQEIYKDLY 443
                                                                                                                                                                                                                                                                        LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL
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                                                                                                                                                                                                                                                                                                                                                                           QSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLAS
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                                                                                                                                                                                                                                            {\tt LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQL}
                                                                                                                                                                                                                                                                                                     LMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVII
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                                                                                                                                                                                      LQVIKKTETDMSLHPLLQEIYKDLY
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                                                                                                                 standard;
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1.9e-167;
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Cytostatic; antiinflammatory; antisense oligonucleotide; PPARgamma;

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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Column 45-48; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antisense compounds capable of modulating expression of peroxisome proliferator-activated receptor gamma useful for diagnosis, prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and treatment of diseases associated with expression of the prophylaxis and the prophylaxis and treatment of diseases associated with expression of the prophylaxis and the prophylaxis a
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nuclear hormone receptor; human; infection; inflammation; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----RNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLR 178
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                                                                                                                                                                                                                                                                                                                                   QSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLAS 298
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87.7%;
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EKTQLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCD
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                                                                                                                                                                                                                                                                                                                            Claim 16;
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N-PSDB; AAH76281.
New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting
                                                                                                                                                                                                                              20-JAN-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                          18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAX8-PPARgamma1; oncogene; cytostatic; PAX8; PPARgamma1; follicular carcinoma; PAX8e7-PPARgammae1; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PAX8e7-PPARgammael protein sequence.
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                                                      peroxisome; cholesterol metabolism; lipid metabolism; respiration;
fatty acid metabolism; beta-oxidation cycle enzyme; hypolipidemic drug;
herbicide; hPPARgamma2; adipose tissue; obesity; diabetes; anorexia;
   hyperlipidaemia;
metabolic disord
                                                                                                      Peroxisome proliferator activated receptor gamma; PPARgamma; human; peroxisome; cholesterol metabolism; lipid metabolism; respiration;
                                                                                                                                                                                                          Peroxisome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCR 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                    proliferator activated receptor gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      λA;
                              hypercholesterolaemia; hyperlipoproteinaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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Pred.
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No. 8
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.8e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               follicular carcinoma
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                              antibody;
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Best Local
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30-JAN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzymes for cholesterol and lipid metabolism, and respiration.

Peroxisome proliferators increase the capacity of the peroxisomes to metabolise fatty acids, via increased expression of the beta-oxidation cycle enzymes. Peroxisome proliferators include unsaturated fatty acids, hypolipidemic drugs, and herbicides. PPARqamma has two main subtypes (hPPARqamma, and hPPARqamma2), which differ in their N-terminal sequences, and are expressed at high levels in adipose tissue. hPPARqamma proteins repress hPPARalpha activity. These proteins can be used in a cell system with a reporter gene (and optionally a hPPARalpha protein) to identify agonists and antagonists of the polypeptides, which can be used as therapeutic agents. The agonists of the polypeptides, which can be used to treat obesity, diabetes, anorexia, hyperlipidaemia, hyperlipidaemia, hyperlipidaemia, hyperlipidaemia, hyperlipidaemia, hyperlipidaemia, hyperlipidaemia, hyperlipidaemia, hyperlipidaemia, and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g. obesity, anorexia and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human peroxisome proliferator activated receptor(s), hPPAR-gamma hPPAR-gamma2 - useful to identify polypeptide (ant)agonists to to
                                                                                                                                                                                                                                                                                                                                                                                                                                                 pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR99323-R99325 represent the three different subtypes of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT35333
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                                                                                                                           146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-1996
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 266
                                257
                                                              206
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                           1996-384114/38
AKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNRDGVLISEGQGFMTREFLKSLRKP
                                                 KTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEY
                                                                                                                           IRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTG
                                                                                                                                                          GFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNA
                                                                                                                                                                                                                                                       PVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYN-----------
                                                                                                                                                                                                                                                                                                                      EMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTD
                                KTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Page 85-87; 108pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               them,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e proliferator activated receptor gamma (hPPARgamma). Thes differ in their N-terminal sequences. Peroxisomes contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                          These sequences, the DNA encoding them, and antibodies in, can be used to establish a tissue specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               hPPARgamma
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0005809.
95US-0380051.
95US-0484487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US01469
                                                                                                                                                                                                                                                                                                                                                                   59.7%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                  Score 2094; DB 17;
Pred. No. 1.2e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                         ----RNKCQYCRFQKCLAVGMSHNA 145
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                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                  Length 494;
                                                                                                                                                                                                                                                                                                                                                      62;
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                                                                                                                                        Query Match
Best Local
                                                                                                                             Matches
                                                                                                                                                                                                  The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX8e8-PPARgammael polypeptide.
                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                     Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BGHM ) BRIGHAM & WOMENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JAN-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAX8-PPARgamma1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PAX8e8-PPARgammae1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB85794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB85794 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  follicular carcinoma;
                          423
                                                                            363
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                                                 88
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                                                                                                                                                                                                                                                                                                                                                                       PAX8-PPARc1 oncogene and oncoprotein,
                                                                                     EMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-514487/56
                        PVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRYCGDKAS
                                      PVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYN-----
                                                                         EMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY
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                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                           certain tumors or cancers, e.g.
                                                                                                                                                                                                                                                                                                                                 Page 106-109; 145pp; English.
                                                                                                                                                                              840
                                                                                                                                                                                                                                                                                                                                                                                                                                     Fletcher
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0177109.
2000US-0225079.
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                                                                                                                                                                             AA;
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                                                                                                                                        59.7%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene; cytostatic; PAX8; PPARgammal;
PAX8e8-PPARgammael; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   840
                                                                                                                        Score 2094; DB 22,
Pred. No. 2.4e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                            follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                       useful for detecting
RNKCQYCRFQKCLAVGMSHNA
                                                                                                                                                  Length
                                                                                                                          Indels
                                                                                                                                                    840;
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RESULT 13
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                                                                                                                                                                                                                                                    23-OCT-1995;
30-JAN-1995;
07-JUN-1995;
                                                                                          Claim 25; ;
                                                                                                                           Human peroxisome proliferator activated receptor(s), hPPAR-gamma hPPAR-gamma2 - useful to identify polypeptide (ant)agonists to to
                                                                                                                                                                                                      Mukherjee
                                                                                                                                                                                                                                                                                                                                                                                                                       Peroxisome proliferator activated receptor gamma; PPARgamma; human; peroxisome; cholesterol metabolism; lipid metabolism; respiration; fatty acid metabolism; beta-oxidation cycle enzyme; hypolipidemic drug; herbicide; hPPARgamma2; adipose tissue; obesity; diabetes; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR99324 standard;
                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                   metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                             hyperlipidaemia;
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                                                                                                                 .g. obesity, anorexia and
                                                                                                                                                                               1996-384114/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEY
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AAR99323-R99325 represent the three different subtypes of human peroxisome proliferator activated receptor gamma (hPPARgamma). These sequences differ in their N-terminal sequences. Peroxisomes contain enzymes for cholesterol and lipid metabolism, and respiration. Peroxisome proliferators increase the capacity of the peroxisomes to metabolise fatty acids, via increased expression of the beta-oxidation peroxisome proliferators include unsaturated fatty

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RESULT 14
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                                                                                                                                                                                                                                     Peroxisome proliferator activated receptor gamma; PPARgamma; human; peroxisome; cholesterol metabolism; lipid metabolism; respiration; fatty acid metabolism; beta-oxidation cycle enzyme; hypolipidemic drug; herbicide; hPPARgamma2; adipose tissue; obesity; diabetes; anorexia; hyperlipidemia; hypercholesterolaemia; hyperlipoproteinaemia; antibody
                                                                                                                           Homo sapiens
                                                                                                                                                                                                           metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peroxisome proliferator activated receptor gamma2 subtype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC AAR99326-R99328 represent the three different subtypes of human CC peroxisome proliferator activated receptor gamma2 (hPPARgamma2). These CS sequences differ in their N-terminal sequences. Peroxisomes contain CC enzymes for cholesterol and lipid metabolism, and respiration. Peroxisome proliferators increased expression of the beta-oxidation CC metabolise fatty acids, via increased expression of the beta-oxidation CC cycle enzymes. Peroxisome proliferators include unsaturated fatty CC acids, hypolipidemic drugs, and herbicides. PARgamma has two main CC subtypes (hPPARgamma, and hPPARgamma2), which differ in their N-terminal CC sequences, and are expressed at high levels in adipose tissue. PPARgamma proteins repress hPPARgamma2), which differ in their Can be used in a cell system with a reporter gene (and optionally a hPPARgahma CC can be used as therapeutic agents. The agonists and antagonists can be used to treat obesity, diabetes, anorexia, hyperlipidaemia, and other metabolic CC disorders. These sequences, the DNA encoding them, and antibodies can be used to treat obesity, diabetes, anorexia, hyperlipidaemia, and onther metabolic constitutes for hepargameas.
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Best Local S
Matches 415
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30-JAN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                  GDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDP
                                                     KSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPF
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                                                                                                                          TTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYA
                                                                                                                                                           TTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYA
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al Similarity
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95US-0484487.
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Pred. No. 2.8e-156;
0; Mismatches 0;
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GDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQ 420

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                                                                                                                                              Query Match
Best Local Similarity 87.0
                                                                                                                                                                                                                                              The invention relates to compounds and ligands that bind to human peroxisome proliferator activated receptors (PPAR) gammal and gamma2. The invention is useful for treating cancer and other disorders including excessive cell proliferation and viral infection. The invention is also directed to the use of PPAR gammal and gamma2 to identify compounds that are antiproliferative, antiviral and antitumour agents. The invention also relates to a method of treating cancer using a pharmaceutical composition comprising thiazolidinedione in an amount sufficient to modulate PPAR gammal and gamma2 activity. The present sequence is human peroxisome proliferator activated receptor (PPAR) gamma1 protein related
                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 2; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Use of thiazolidinedione for treating cancer and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith RG;
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18-APR-1997;
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                                                                                                                                                                                                                                          the invention.
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                                                                 MTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDP
                                                                                                                  MTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDP 88
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DB; AAD21021.
                                                 VVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASG
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97US-0844007.
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87.0%;
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           LKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 443
                                                          GDFMEPKFEFAVKFNALELDDSDLAIFTAVIILSGDRPGLLNVKPIEDIQDNLLQALELQ
LKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 477
                                            GDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQ
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Search completed: February 25, 2003, 03:58:26
Job time: 65 secs

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SUMMARIES

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Minimum
Maximum
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-O=/cgn2_1/USPTO_spool/US09931007/runat_14022003_102553_4668/app_query.fasta_1.839
-DB=N_Geneseq_101002 -OFMT=fastap -SUFFIX=p2n.rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTEMT=pto -NORM=ext -HRAFSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09931007_eGGN_1_1_236_evrunat_14022003_102553_4668 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Ygapop 10.0 , Ygapext
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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  Location/Qualifiers
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Human; peroxisome proliferator activated receptor gamma2; PPAR gamma2; cytotoxic; antiproliferative; antiviral; cancer; cell proliferation; viral infection; pharmaceutical; thiazolidinedione; ss.

Human peroxisome proliferator activated receptor (PPAR) gamma2 cDNA

15-JAN-2002 (first entry)

RESULT 1 AAD21022

AAD21022 standard;

cDNA; 1518

ALIGNMENTS

Result No. O C 2094
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11076.5 2231 2106.5 2106.5 2099 2098 Score Query Match  $\begin{array}{c} 663.6\\ 63.6\\ 663$ Length DB 2635 2336 2536 2536 2523 2523 11811 1647 2596 IJ AAF30517 AAQ92081 AAT16206 ABN95714 AAF55663 AAS44653 AAX25481 AAD21021 AAX36522 AAH76296 AAI07275 ABS14765 AAQ39089 AAX19070 AAX36523 ABL65244 AAT10583 AAQ48939 AAH76283 AAH76281 AAT35334 AAH76294 AAH33499 AAH76282 AAT35333 AAH76288 AAD21022 Peroxisome prolife
Steroid hormone re
Human PpAR-delta c
Lung cancer relate
Peroxisome prolife
Human peroxisome p
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                                                                                                                                                                                                                                                                                                                                                                                           US-09-931-007A-1 (1-688) x AAD21022 (1-1518)
                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to compounds and ligands that bind to human peroxisome proliferator activated receptors (PPAR) gammal and gamma2. The invention is useful for treating cancer and other disorders including excessive cell proliferation and viral infection. The invention is also directed to the use of PPAR gammal and gamma2 to identify compounds that are anniproliferative, antiviral and antitumour agents. The invention also relates to a method of treating cancer using a pharmaceutical composition comprising thiazolidinedione in an amount sufficient to modulate PPAR gammal and gamma2 activity. The present cDNA sequence encodes human peroxisome proliferator activated receptor (PPAR) gamma2 protein related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith
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18-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 3; 17pp; English.
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                                                                                                                                                                                                                                                 of thiazolidinedione for treating cancer and
GlnLeuTyrAsn--
                                GluTyrGlnSerAlaIleLysValGluProAlaSerProProTyrTyrSerGluLysThr 120
                                                             LeuSerAlaAsnIleSerGlnGluMetThrMetValAspThrGluMetProPheTrpPro 40
                                                                                                                                                                                                                                       ATGGGTGAAACTCTGGGAGATTCTCCTATTGACCCAGAAAGCGATTCCTTCACTGATACA
                       GAGTACCAAAGTGCAATCAAAGTGGAGCCTGCATCTCCACCTTATTATTCTGAGAAGACT
                                                                                                                                                                                            CTGTCTGCAAACATATCACAAGAAATGACCATGGTTGACACAGAGATGCCATTCTGGCCC
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97US-0844007.
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/product= "Human peroxisome proliferator activated
/product (PPAR) gamma2 protein"
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87.72%
63.60%
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438	LeuGlnVall1LeLysLysThrCluThrAspMetSerLeuHisProLeuLeuGlnGluIle	419	Qy
1440	CTGCTCCAGAAATGACAGACCTCAGACAGATTGTCACGGAACACGTGCA	1381	Db
418	laLysLeuLeuGlnLysMetThrAspLeuArgGlnIleValThrGluHisValGlnLe	399	Qy
398 1380	LeuLeuGlnAlaLeuGluLeuGlnLeuLysLeuAsnHisProGluSerSerGlnLeuPhe	379 1321	Оу
w		1261	Db
378	euSerGlyAspArgProGlyLeuLeuAsnValLysProIleGluAspIleGlnAspA	359	Qy
1260	TTCAA	1201	Db
358	sPheAsnAlaLeuGluLeuAspAspSerAspLeuAlaIlePheIleAlaValIleIl	339	Qy
1200	AGAGCCTGCGAAAGCCTTTTGGTGACTTTATGGAGCCCAAGTTTGAGTTTGCTG	1141	Db
338	euLysSerLeuArgLysProPheGlyAspPheMetGluProLysPheGluPheAlaVa	319	Qy
1140	GATGAATAAAGATGGGGTTCTCATATCCGAGGGCCAAGGCTTCATGACAAGGGAGT	1081	DЬ
318	euMetAsnLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPh	299	Qy
1080	GTAACTCTCCTCAAATATGGAGTCCACGAGATCATTTACACAATGCT	1021	DЬ
298	spGlnValThrLeuLeuLysTyrGlyValHisGluIleIleTyrThrMetLeuAlaSe	279	Qy
1020	CAGGAGATCACAGAGTATGCCAAAAAGCATTCCTGGTTTTGTAAATCTTGACTTGAA	961	Db
278	alGlnGluIleThrGluTyrAlaLysSerIleProGlyPheValAsnLeuAspLeuA	259	Qy
960	TCGCTCCGTGGAGGC	901	DЪ
258	lnSerLysGluValAlaIleArgIlePheGlnGlyCysGlnPheArgSerValGluA	239	Qy
900	GTTCAAACACATCACCCCCCTGCAGGA	841	Db
238	snSerLeuMetMetGlyGluAspLysIleLysPheLysHisIleThrProLeuGlnG	219	Qy
840	GCGATCTTGACAGGAAAGACAACAGACAAATCACCATTCGTTATCTA	781	Db
218	laArgAlaIleLeuThrGlyLysThrThrAspLysSerProPheValIleTyrAsp	199	Qy .
780	GCAAAACATTTGTATGACTCATACATAAAGTCCTTCCCGCTGACCAAAGCAAA	721	Дb
198	laLeuAlaLysHisLeuTyrAspSerTyrIleLysSerPheProLeuThrLysAl	179	Оу
720	TIGGCGGAGATCTCCAGTGATATCGACCAGCTGAATCCAGAGTCCGCTGACCTCCG	661	Db
178	euLeuAlaGluIleSerSerAspIleAspGlnLeuAsnProGluSerAlaAspLeuA	159	Qy
660	CATAATGCCATCAGGT	601	Db
158	alGlyMetSerHisAsnAlaIleArgPheGlyArgMetProGlnAlaGluLysGluLy	139	Qy
600	GTCAGTACTGTCGGTTTCAGAAAT	541	Db
138	gAsnLysCysGlnTyrCysArgPheGlnLysCysLeuAl	125	Qу
540	GGTTTCTTCCGGAGAACAATCAGATTGAAGCTTATCTATGACAGATGTGATCTTAACTGT	481	Db
124		124	Qy
480	GTCTGTGGAGATAAAGCTTCTGGATTTCACTATGGAGTTCATGCTTGTGAAGGATGCAAG	421	Db
124		124	Qy
420		361	Db

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RESULT 2
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XX AAH76288
AC AAH7
XX AAH76288
AC AAH7
XX AAH7628
AC AAH7
XX AAH7629
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                                                                                                                 US-09-931-007A-1 (1-688)
                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a
                                                                                                                                                                                                                                                                                                                                                           subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New
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14-AUG-2000;
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                                     sapiens
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 LeuSer \verb|AlaAsnIleSerGlnGluMetThrMetValAspThrGluMetProPheTrpPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-514487/56.
B; AAB85800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fletcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 123-125; 145pp;
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2000US-0225079
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                                                                                                                                                                                                                                                                                                                                            represents a human PPARgamma
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2231.00
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LeuLysSerLeuArgLysProPheGlyAspPheMetGluProLysPheGluPheAlaVal
                                                                            LeuMetAsnLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPhe
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                                                                                                                                                    AspGlnValThrLeuLeuLysTyrGlyValHisGluTleTleTyrThrMetLeuAlaSer
                                                                                                                                                                                                                                                                                                                                                                               AsnSerLeuMetMetGlyGluAspLysIleLysPheLysHisIleThrProLeuGlnGlu
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                                                        TTGATGAATAAAGATGGGGTTCTCATATCCGAGGGCCAAGGCTTCATGACAAGGGAGTTT
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  associated
           specifically hybridises with and inhibits the expression of human PPARgamma. The present sequence is the coding sequence for human PPARgamma artisense oligonucleotides of the present invention can be used in the diagnosis and treatment of diseases
                                                   Peroxisome proliferator-activated receptors (PPARs) are members of the nuclear hormone receptor subfamily of transcription factors. The present invention relates to antisense oligonucleotides (see AAP33652-F23731), targeted to a nucleic acid molecule encoding human PPARgamma, which
                                                                                                       Example 13;
                                                                                                                                   Novel antisense compounds capable of modulating expression of peroxisome proliferator-activated receptor gamma useful for diagrophylaxis and treatment of diseases associated with expression
                                                                                                                                                                                                          McKay
                                                                                                                                                                                                                              (ISIS-)
                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                    Cytostatic; antiinflammatory; antisense oligonucleotide; PPARgamma; peroxisome proliferator-activated receptor gamma; transcription factor; nuclear hormone receptor; human; infection; inflammation; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                               Human PPARgamma
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AsnSerLeuMetMetGlyGluAspLysIleLysPheLysHisIleThrProLeuGlnGlu
                                           GCGAGGGCGATCTTGACAGGAAAGACAACAGACAAATCACCATTCGTTATCTATGACATG
                                                        AlaArgAlaIleLeuThrGlyLysThrThrAspLysSerProPheValIleTyrAspMet
                                                                                                    GCCCTGGCAAAACATTTGTATGACTCATACATAAAGTCCTTCCCGCTGACCAAAGCAAAG
                                                                                                                 AlaLeuAlaLysHisLeuTyrAspSerTyrIleLysSerPheProLeuThrLysAlaLys
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                                                                                                                 Peroxisome proliferator activated receptor gamma; PPARgamma; human; peroxisome; cholesterol metabolism; lipid metabolism; respiration; fatty acid metabolism; beta-oxidation cycle enzyme; hypolipidemic drug; herbicide; hPPARgamma2; adipose tissue; obesity; diabetes; anorexia; hyperlipidaemia; hypercholesterolaemia; hyperlipoproteinaemia; antibody; metabolic disorder; therapy; ss.
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                                      /*tag= a
/product=
214..1647
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220..1647
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Query Match:
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Best Local Similarity:
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30-JAN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peroxisome proliferator activated receptor(s), hPPAR-gamma and hPPAR-gamma2 - useful to identify polypeptide (ant)agonists to treat
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Percent Similarity: Best Local Similarity:

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Length:
Matches:
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                                             The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamman ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-pPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX8e9(-exon 8)-PPARgammael polypeptide encoding cDNA.
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14-AUG-2000;
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New PAX8-PPARcl oncogene and oncoprotein, useful for detecting treating certain tumors or cancers, e.g. follicular carcinoma
                                                         WPI; 2001-514487/56.
P-PSDB; AAB85795.
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14-AUG-2000;
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains a PAX8 coding region fused to PPÁRgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX8e9-PPARgammael polypeptide
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AAGGAGAAGCTGTTGGCGGAGATCTCCAGTGATATCGACCAGCTGAATCCAGAGTCCGCT
                                                                    TGCCTTGCAGTGGGGATGTCTCATAATGCCATCAGGTTTTGGGCGGATGCCACAGGCCGAG
                                                                                     CysLeuAlaValGlyMetSerHisAsnAlaIleArgPheGlyArgMetProGlnAlaGlu
                                                                                                                                         CTTAACTGTCGGATCCACAAAAAAAGTAGAAATAAATGTCAGTACTGTCGGTTTCAGAAA
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30-JAN-1995;
07-JUN-1995;
expression of the beta-oxidation cycle enzymes. Peroxisome proliferate include unsaturated fatty acids, hypolipidemic drugs, and herbicides. PPARgamma has two main subtypes (hPPARgamma, and hPPARgamma2), which differ in their N-terminal sequences, and are expressed at high levels adipose tissue. hPPARgamma proteins repress hPPARalpha activity. The encoded proteins can be used in a cell system with a reporter gene (and optionally a hPPARalpha protein) to identify agonists and antagonists can be used as therapeutic agents. The agonists and antagonists can be used to treat obesity, diabetes, anorexia,
                                                                                                                                                                                                                                                                                                                     proliferator activated receptor gamma (hPPARgamma). This sequence encodes three different hPPARgamma subtypes, which differ in their N-terminal sequences. Peroxisomes contain enzymes for cholesterol and lipid metabolism, and respiration. Peroxisome proliferators increased capacity of the peroxisomes to metabolise fatty acids, via increased capacity of the peroxisomes to metabolise fatty acids, via increased
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         AspLysIleLysPheLysHisIleThrProLeuGlnGluGlnSerLysGluValAlaIle
                                               LysThrThrAspLysSerProPheValIleTyrAspMetAsnSerLeuMetMetGlyGlu
                                                                                                                                                                                                   AsnLysCysGlnTyrCysArgPheGlnLysCysLeuAlaValGlyMetSerHisAsnAla
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           AsnLysCysGlnTyrCysArgPheGlnLysCysLeuAlaValGlyMetSerHisAsnAla
                                                     AGATTGAAGCTTATCTATGACAGATGTGATCTTAACTGTCGGATCCACAAAAAAAGTAGA 1566
                                                                                                             GGATTTCACTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTCTTCCGGAGAACAATC 1506
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            peroxisome proliferator
  antiproliferative;
                                                         (first entry)
                                                                                                        cDNA;
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 cactivated antiviral;
receptor gamma1; PPAR gamma
cancer; cell proliferation;
                                  gamma1
            gamma1;
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                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                               excessive cell proliferation and viral infection. The invention is also directed to the use of PPAR gammal and gamma2 to identify compounds that are antiproliferative, antiviral and antitumour agents. The invention also relates to a method of treating cancer using a pharmaceutical composition comprising thiazolidinedione in an amount sufficient to modulate PPAR gammal and gamma2 activity. The present cDNA sequence encodes human peroxisome proliferator activated receptor (PPAR) gammal protein related to the invention.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to compounds and ligands that bind to human peroxisome proliferator activated receptors (PPAR) gammal and gamman the invention is useful for treating cancer and other disorders in the invention is useful for treating cancer.
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18-APR-1997;
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            GluProAlaSerProProTyrTyrSerGluLysThrGlnLeuTyrAsn---
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                                                 GTGGTTGCAGATTACAAGTATGACCTGAAACTTCAAGAGTACCAAAGTGCAATCAAAGTG
                                                            ValValAlaAspTyrLysTyrAspLeuLysLeuGlnGluTyrGlnSerAlaIleLysVal 108
                                                                                                  GACTTCTCCAGCATTTCTACTCCACATTACGAAGACATTCCATTCACAAGAACAGATCCA
                                                                                                              AspPheSerSerIleSerThrProHisTyrGluAspIleProPheThrArgThrAspPro
                                                                                                                                                  GATCTCTCCGTAATGGAAGACCACTCCCACTCCTTTGATATCAAGCCCTTCACTACTGTT
                                                                                                                                                               AspLeuSerValMetGluAspHisSerHisSerPheAspIleLysProPheThrThrVal
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DB; AAE12867.
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                              GGTGACTTTATGGAGCCCAAGTTTGAGTTTGCTGTGAAGTTCAATGCACTGGAATTAGAT
                                                                                                                                                                                                 GGAGTCCACGAGATCATTTACACAATGCTGGCCTCCTTGATGAATAAAGATGGGGTTCTC
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        AspLeuArgGlnIleValThrGluHisValGlnLeuLeuGlnValIleLysLysThrGlu
                                                                                                                                                                  ATATCCGAGGCCCAAGGCTTCATGACAAGGGAGTTTCTAAAGAGCCTGCGAAAGCCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for identifying nuclear receptor agonists and antagonists comprises measuring fluorescent resonance transfer between fluorescent-labelled nuclear receptors and co-activators. The method can be used for identifying agonists and antagonist of nuclear receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
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CTACAAGCCCTGGAGCTCCAGCTGAAGCTGAACCACCCTGAGTCCTCACAGCTGTTTGCC
        LeuGlnAlaLeuGluLeuGlnLeuLysLeuAsnHisProGluSerSerGlnLeuPheAla
                                                                    SerGlyAspArgProGlyLeuLeuAsnValLysProIleGluAspIleGlnAspAsnLeu
                                                                                                                                           CAGGAGATCACAGAGTATGCCAAAAAGCATTCCTGGTTTTGTAAATCTTGAACTTGAACGAC
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Alignment Pred. No.: Score:

No.:

Best 1 Query DB:

Percent Similarity:
Best Local Similarity:
Query Match:

4.95e-182 2065.50 85.71% 84.49% 58.88%

Length:
Matches:
Conservative:
Mismatches:

US-09-931-007A-1 (1-688) x

AAH76296

(1-1811)

Indels: Gaps:

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                    The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PPARgamma polypeptide encoding cDN
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Sequence
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14-AUG-2000;
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follicular carci
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                                    MetAsnLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPheLeu
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                                                                                     The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocallular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of
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expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detectin the progression of liver cancer, hepatocellular carcinoma and methods.

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated and purified polynucleotide encoding human proliferator-activated receptor gamma polypeptide useful idiagnostics, drug design and therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a human peroxisome proliferator activated receptor gamma (PPAR-gamma) polypeptide. PPAR are orphan receptors, and may play a role in proliferative and differentiation aspects of cancer. The PPAR-gamma polypucleotide is useful for detecting a mRNA transcript that encodes PPAR polypeptide. It is also useful for detecting hybrid formation. The PPAR-gamma polypeptide is useful in diagnostics, drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1844 BP;
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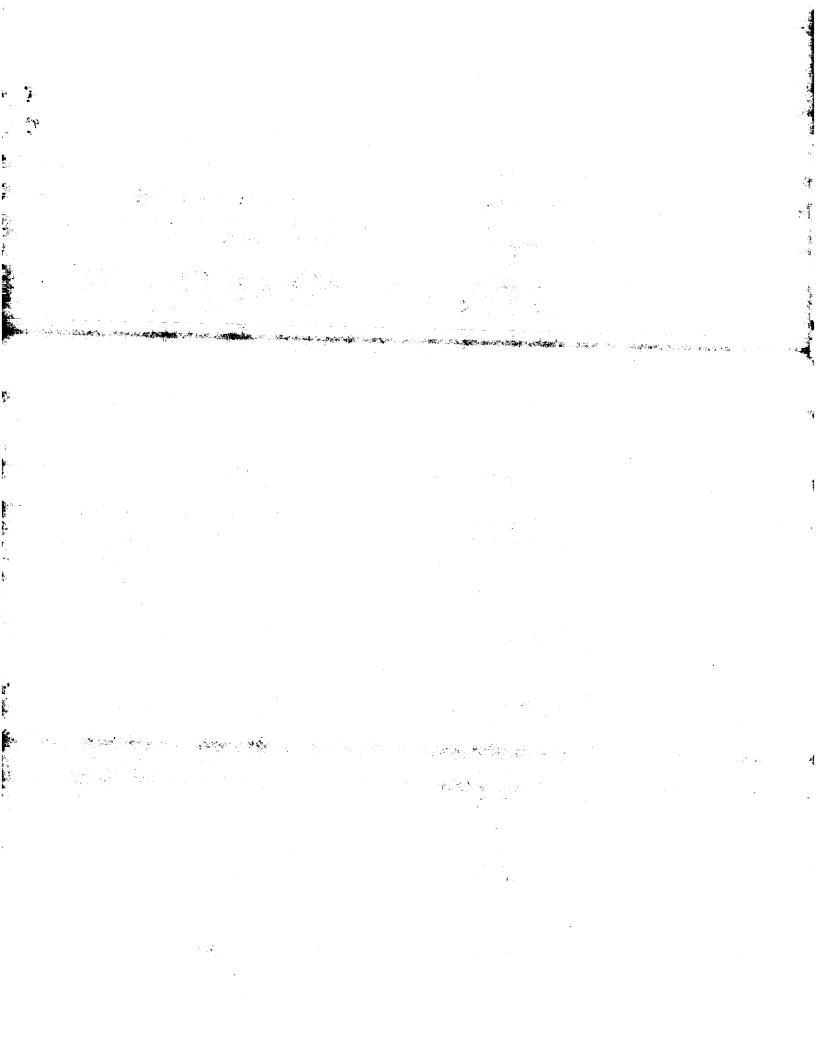
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Best Local Similarity:
Query Match:
DB:
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18-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                as multiple sclerosis, connective tissue disease, rheumatoid arthritis, disbates mellitus, allergic rhinitis, asthma and eczema, nervous system disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to alsorders. The sequences may also be used for regeneration of bone, as a contract of the deal of the contract and then be sequenced may also be used for regeneration of bone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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                                    GlnGluIleThrGluTyrAlaLysSerIleProGlyPheValAsnLeuAspLeuAsnAsp
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            MetAsnLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPheLeu
                                                                                      CAGGAGATCACAGAGTATGCCAAAAGCATTCCTGGTTTTGTAAATCTTGACTTGAACGAC
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh

-Q-gcn2_1/USPTO_Spool_US09931007/runat_14022003_102553_4687/app_query.fasta_1.839

-DB-EST -QFMT-fastap -SUFFIX-p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45

-DCCALIGN=200 -THR_SCORE-pct -THR_MAX100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=20000000

-USER-GS09931007_8CGN 1_1_1698_@runat_14022003_102553_4687 -NCPU=6 -ICPU=3

-NO_XID-XY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , X
Fgapop 6.0 , F
Delop 6.0 , I
February 25, 2003, 04:02:01; Search time 2471 Seconds (without alignments) 4509.306 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

TITLE	SACHEIM	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AL549707/c	RESULT 1
Full-length cDNA libraries and normalization	I W B Gruber C Jessee I and Bolaves D	1 (bases 1 to 961)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens ,	human .	EST	AL549707.1 GI:12885958	AL549707	prime, mRNA sequence.	AL549707 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI055YI11 3	AL549707 961 bp mRNA linear EST 16-FEB-2001		

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                              sAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPheLeuLysSerLe 322
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                                                                                                      AGATGGGGTTCTCATATCCGAGGGCCAAGGCTTCATGACAAGGGAGTTTCTAAAGAGCCT
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Email: seqref@genoscope.cns.fr, '
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Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: FINANSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"

a 216 c 236 g 267 t 16 others
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/tissue_type="placenta"
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/db_xref="taxon:9606"
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Email:
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Contact: Genoscope
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/tissue_type="placenta"

/note="Vector: pCMVSPORT 6: Site_1: NotI; 1st strand cDNA

/note="Vector: pCMVSPORT 6: Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact: Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                            http://fulllength.invitrogen.com"
196 c 208 g 239 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CS0DI006YI10"
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/db_xref="taxon:9606"
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QΥ

LeuArgAlaLeuAlaLysHisLeuTyrAspSerTyrIleLysSerPheProLeuThrLys 196

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/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
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Contact: Genoscope Genoscope - Centre National de Sequencage
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/clone="CSODIO28YJ24"
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                                                                                                                                                Li, W.B., Gruber, C., Jessee, J. and Polayes.
Full-length cDNA libraries and normalizat:
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                     BP 191
Email:
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segref@genoscope.cns.fr,
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                             /sex="male"
                                                           /db_xref="taxon:9606"
/clone="CS0DC004Y008"
                                           /clone_lib="LTI_NFL003_NBC3"
                                                                                       /organism="Homo sapiens"
                                                                                                                     Location/Qualifiers
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EST 13-FEB-2001

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Score:

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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602633578F1 NCI_CGAP_Skn3
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1 (bases 1 to 793)
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/site_2: Sall; Cloned unidirectionally. Primer:
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a 176 c 195 g 193 t 1 others
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/clone="IMAGE:4778658"
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RESULT 7
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                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                               Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 826)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM8415 row: k column: 13
High quality sequence stop: 736.
Location/Qualifiers
                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
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EST.
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BE535401
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                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3445380"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ:
Site_2: SalI;
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Eutheria; Primates; Catarrhini; Hominidae;
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Best Local Similarity:
Query Match:
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32.38%
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Qy 152	Db 303		Qy 125	Db 183	Qy 124	Db 123	QY 124	Db 63	us-09-931-	Alignment Pred. No.: Score: Percent Si Best Local Query Matc DB:	BASE COUNT	source	FEATURES	COMMENT	AUTHORS TITLE	CRGANION	VERSION KEYWORDS SOURCE	ACCESSION	LOCUS
ProGlnAlaGluLysGluLysLeuLeuAlaGluIleSerSerAspIleAspGlnLeuAsn 171	ArgPneGinLyscysLeuAlaValGlyMetSerHisAsnAlaIleArgPheGlyArgMet 151 	OUNCOUNT OF TOUR CETTER A TOUR OF TOUR OF TOUR OF THE TOUR OF TOUR OF THE TOUR	ArgAsnLysCysGlnTyrCys 131	CATGCTTGTGAAGGATGCAAGGGTTTCTTCCGGAGAACAATCAGATTGAAGCTTATCTAT 242	124	CTCATGGCAATTGAATGTCGTGTGTGGAGATAAAGCTTCTGGATTTCACTATGGAGTT 182	124	ProTyrTyrSerGluLysThrGlnLeuTyrAsn	-007A-1 (1-688) x AL549611 (1-900)	Alignment Scores:  2.72e-132	20 66 a TH 70 L 4 C 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		BP 191 91006 EVRY Email: segref@geno;		Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization	د,		prime, mRNA sequence.	AL549611 TI NFL006 PL2 Homo sapiens cDNA clone CS0DI055VII1 5

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                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG179310 1088 bp mRNA linear EST 06-FF 602331030F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4432278 mRNA sequence.
BG179310
BG179310.1 GI:12686013
EST.
                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10188 row: 1 column: 07
High quality sequence stop: 658.
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1088)
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: No
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:4432278"
/clone_lib="NIH_MGC_91"
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Email: segref@genoscope.cns.fr, Web : www
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B0883138
                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 944)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM13578 row:
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                                                                                                                      e: LLAM13578 row: j column: 11 quality sequence stop: 707. Location/Qualifiers
                                                 /organism="Homo sapiens"
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/clone="IMAGE:6186346"
/clone_lib="Lupski_dorsal_root_ganglion
/sex="male"
                        /tissue_type="dorsal root
/dev_stage="adult, 36 yr"
          /dev_stage="adult, 36
/lab_host="DH10B"
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
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Full-length cDNA libraries
Unpublished (2001)
Contact: Genoscope
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                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ722874 872 bp mRNA linear EST AGENCOURT_8099880 Lupski_sympathetic_trunk Homo sapiens IMAGE:6190020 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
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                                                                                          quality sequence stop:
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                   Location/Qualifiers
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Primates;
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Pred. No.:
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                                                                                                                                                                                                                                 AlaIleArgIlePheGlnGlyCysGlnPheArgSerValGluAlaValGlnGluIleThr
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               euArgLysProPhe---GlyAspPheMetGluPro 332
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                                                        GGGGTTCTCATATCCGAGGGGCCAGGGCCTTCATGGACAAGGGAGTTTTCTAAAAGAGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
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/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
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               GATATCAAGCCCTTCACTACTGTTGACTTCTCCAGCATTTCTACTCCACATTACGAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: pooled brain, lung, testis; Vector: /note="Organ: pooled brain, lung, testis; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5175351"
/clone=lib="NIH_MGC_115"
/lab_host="DH10B"
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AL549037 LTI_NFL006_PL2 H
Prime, mRNA sequence.
AL549037
AL549037.1 GI:12884632
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                        Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
Unpublished (2001)
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Rockville, Maryland 20850, USA Fax: Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                         /tissue_type="placenta"
/note="Vector: pCMVSPOR'
                                                                                                                                                   /clone="CS0DI042YB22"
/clone_lib="LTI_NFL006_PL2"
                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Search completed: February 25, 2003, 06:13:34
Job time: 2484 secs

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bitsum62
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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     2231
2196.5
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/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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     1608
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2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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  US-09-765-111A-15
US-10-109-886-5
US-09-765-111A-22
US-09-765-111A-5
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1415.414 Million cell updates/sec
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Sequence 15, Appli
Sequence 5, Appli
Sequence 22, Appli
Sequence 5, Appli
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## ALIGNMENTS

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US-09-765-111A-15
Sequence 15, Application US/09765111A
Patent NO. US20020106796A1
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: FIetcher, JONATHAN A.
APPLICANT: FITCH OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/EPF/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
FRIOR APPLICATION NUMBER: US 60/225,079
CONTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 1608
TYPE: DNA
ORGANIAM: Homo Sapiens
PRIOR APPLICATION: (91)...(1608)
US-09-765-111A-15
Alignment Scores:
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OO MATCHES: CONSERVATIVE: OAS MISMATCHES: OAS MISMATCHES: OAS AND MISMATCHES: OAS BE GAPS: 1-09-765-111A-15 (1-1608) SpSerProILeAspProGluSerAspSeli	Qy 239 GlnSerLySGluValAlaI	Qy 219 AsnSerLeuMetMetGlyG 	Qy 199 AlaArgAlaIleLeuThrG	Qy 179 AlaLeuAlaLySHiSLeuTy	Qy 159 LeuLeuAlaGluIleSerS	Qy 139 ValGlyMetSerHisAsnA 	Qy 125Ar	Db 571 GGTTTCTTCCGGAGAACAATC	Qy 124	511 GTCTGTGGAGATAAAGCTT	.24	Qy 121 GlnLeuTyrAsn	Db 391 GAGTACCAAAGTGCAATCA	luTyrGlnSerA	Qy 81 IleProPheThrArgThrA                     1	Qy 61 ASPI1eLysProPheThTT 	CCAACTTTGGGATCAGCT	GlyIleSerS	Qy 21 LeuSerAlaAsnIleSerG 	Qy 1 MetGlyGluThrLeuGlyA 	US-09-931-007A-1 (1-688) x US	Score: 2231. Score: 87.72 Percent Similarity: 87.72 Best Local Similarity: 87.72 Query Match: 63.60 DB: 10
	eArgIlePheGlnGlyCysGlnPheArgSerValGluAl 	uAspLysIleLysPheLysHisIleThrProLeuGlnGl 	yLysThrThrAspLysSerProPheVallleTyrAspMe 	rAspSerTyrIleLysSerPheProLeuThrLysAlaLy 	rAspIleAspGlnLeuAsnProGluSerAlaAspLeuAr 	alleArgPheGlyArgMetProGlnAlaGluLysGluLy 	gAsnLysCysGlnTyrCysArgPheGlnLysCysLeuAl 	agattgaagcttàtctatgacagatgtgatcttaactg		TGGATTTCACTATGGAGTTCATGCTTGTGAAGGATGC <i>P</i>		TGAAGAGCCTTCCAACTCCCTCATGGCAATTGAATGTCG	CCTGCATCTCCACCTTATTATTCTGAGAAGAC	ProAlaSerProProTyrTyrSerGluLysTh	ValAlaAspTyrLysTyrAspLeuLysLeuG 	ValaspPheSerSerIleSerThrProHisTyrGlua 	CGTGGATCTCTCCGTAATGGAAGACCACTCCCACTCCTT	rValAspLeuSerValMetGluAspHisSerHisSerPh	GlumetThrmetValAspThrGlumetProPheTrpPr 	SerProIleAspProGluSerAspSerPheThrAspTh 	09-765-111A-15 (1-1608	0 Matches: 4 Conservative: 0 Mismatches: 6 Indels: 6 Gaps: 1

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CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT FILLNG DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 09/514,247
PRIOR APPLICATION NUMBER: 09/514,247
PRIOR PPLICATION NUMBER: 07/1998/03734
PRIOR FILLNG DATE: 1998-08-24
PRIOR FILLNG DATE: 1998-08-24
PRIOR FILLNG DATE: 1998-08-24
PRIOR FILLNG DATE: 1998-08-24
PRIOR FILLNG DATE: 1998-08-27
PRIOR FILLNG DATE: 1999-08-27
PRIOR FILLNG DATE: 1997-08-27
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PRIOR FILLNG DATE: 1997-08-27
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US-10-109-886-5
                                                                                                                                                                                                                                                                          Sequence 5, Application US/10109886
Patent NO. US20020119499A1
GEMERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: MANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING
TITLE OF INVENTION: ANTAGONIST TO PPAR
                                                                                                                                  SOFTWARE: 1
SEQ ID NO 5
                                                         NAME/KEY: CDS
LOCATION: (15
                                                                                 ORGANISM: Homo sapiens FEATURE:
                                                                                                         TYPE: DNA
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                                 GluGlnSerLysGluValAlaIleArgIlePheGlnGlyCysGlnPheArgSerValGlu
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Query Match:
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APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
TITLE OF INVENTION: PAX8-PPARGAMMA NUC
TITLE OF INVENTION: AND POLYPEPTIDES
FILE REFERENCE: B0801/7195/ERP/MAT
FILE REFERENCE: B0801/7195/ERP/MAT
                                                                                                                                                              SEQ ID NO 22
LENGTH: 2596
                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09765111A Patent No. US20020106796A1
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/765,111A CURRENT FILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: US 60/177,109 PRIOR FILING DATE: 2000-01-20 PRIOR APPLICATION NUMBER: US 60/225,079 PRIOR FILING DATE: 2000-08-14 NUMBER OF SEQ ID NOS: 47 NUMBER: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                         ORGANISM: Homo
                                                                                                                                                     TYPE: DNA
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                                                    GTGGAGGCTGTGCAGGAGTACACAGAGTATGCCAAAAGCATTCCTGGTTTTGTAAATCTT
                                                                  ValGluAlaValGlnGluIleThrGluTyrAlaLysSerIleProGlyPheValAsnLeu
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Best Local Similarity:
Query Match:
DB:
                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)...
US-09-765-111A-5
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US-09-931-007A-1 (1-688) x US-09-765-111A-5 (1-2625)
                                                        Percent Similarity:
                                                                                             Alignment Scores
                                                                                                                                                                             SOFTWARE: FASTSEQ for Windows
SEQ ID NO 5
LENGTH: 2625
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09765111A Patent No. US20020106796A1
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC TITLE OF INVENTION: AND POLYPEPTIDES AND UFILE REFERENCE: B0801/7196/ERP/MAT CURRENT APPLICATION NUMBER: US/09/765,111A CURRENT FILING DATE: 2001-01-18
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PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                      LeuGlnGluGlnSerLysGluValAlaIleArgIlePheGlnGlyCysGlnPheArgSer
                                                                                                                                                                       TyrAspMetAsnSerLeuMetMetGlyGluAspLysIleLysPheLysHisIleThrPro
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                                                                                                                     CTGCAGGAGCAGAGCAAAGAGGTGGCCATCCGCATCTTTCAGGGCTGCCAGTTTCGCTCC
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GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Froil, Todd G.
TITLE OF INVENTION: PAX8-PPARGAMMA NUCLEIC ACI
TITLE OF INVENTION: AND POLYPEPTIDES AND USEE
FILE REFERENCE: B0801/7196/FRP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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US-09-765-111A-1
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US-09-765-111A-1
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                                                              MetAsnLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPheLeu
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                                                     ATGAATAAAGATGGGGTTCTCATATCCGAGGGCCAAGGCTTCATGACAAGGGAGTTTCTA
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Sequence 3, Application US/09765111A

Patent No. US20020106796A1

GENERAL INFORMATION:

APPLICANT: Fletcher, Jonathan A.

APPLICANT: Kroll, Todd G.

TITLE OF INVENTION: PAAB-PPARGamma NUCLEIC ACID MOLECULES

TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: B0801/7196/ERP/MAT

CURRENT APPLICATION NUMBER: US/09/765,111A

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/177,109

PRIOR APPLICATION NUMBER: US 60/177,109

PRIOR APPLICATION NUMBER: US 60/225,079

PRIOR FILING DATE: 2000-01-20

PRIOR FILING DATE: 2000-08-14

NUMBER OF SEQ ID NOS: 47

SOFTMARE: FastSEQ for Windows Version 3.0
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Best Local Similarity:
Query Match:
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; LOCATION: (1)...(2523)
US-09-765-111A-3
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LENGTH: 2523
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Qy 124	386 GlnLeuLysLeuAsnHisProGluSerSerGlnLeuPheAlaLysLeuLeuGlnLysMet 405	Qy
Db 455 TAC	2287 TTGCTGAATGTGAAGCCCATTGAAGACATTCAAGACAACCTGCTACAAGCCCTGGAGCTC 2346	Дb
Qу 123 Туј	366 LeuLeuAsnValLysProIleGluAspIleGlnAspAsnLeuLeuGlnAlaLeuGluLeu 385	Qy
Qy 103 Glr 	346 AspAspSerAspLeuAlaIlePheIleAlaValIleIleLeuSerGlyAspArgProGly 365 	Qу
Qy 83 Phe 		Db
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Score: Score: Score: Percent Simi Pert Local S: Ouery Match:	226 ASPLYSIIeLYSPheLYSHiSIIeThrProLeuGlnGluGlnSerLYSGluValAlaIle 245	Qy Db
US-09-765-111 Alignment Sco	206 LysThrThrAspLysSerProPheVallIeTyrAspMetAsnSerLeuMetMetGlyGlu 225 	Qу
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PRIOR FILL PRIOR FILL PRIOR FILL NUMBER OF	146 IleArgPheGlyArgMetProGlnAlaGluLysGluLysLeuLeuAlaGluIleSerSer 165 	Qy Db
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RESULT 7	1387 GAAGAGCCTTCCAACTCCCTCATGGCAATTGAATGTCGTGTGTGGGAGATAAAGCTTCT 1446	Db
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LING DATE: 2000-01-20
PLICATION UNMBER: US 60/225,079
LING DATE: 2000-08-14
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T: Kroll, Todd G.
INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
INVENTION: AND POLYPEPTIDES AND USES THEREOF
ERENCE: B0801/7196/ERP/MAT
APPLICATION NUMBER: US/09/765,111A
FILING DATE: 2001-01-18
FILING DATE: 2001-01-18
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FastSEQ for Windows Version
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US20020106796A1
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APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950 SOFTWARE: PALENTIN VOT: 2.1 SEQ ID NO 2212 LENGTH: 1811
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Query Match:
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Best Local Similarity:
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US-09-880-107-2212
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APPLICANT: Horne,
APPLICANT: Vockle,
APPLICANT: Scherf,
APPLICANT: Gene L
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Scherf, Uwe
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US-09-816-828-8/c
; Sequence 8, Application US/09816828
; Patent No. US20020150898A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
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TENGTH: 2260
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CURRENT FILING DATE: 2001-03-22
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TITLE OF INVENTION: No. US20020150898A1e1
TITLE OF INVENTION: Polypeptides
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Ma, Yunqing
Wang, Zhiwei
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Wang, Jian-Rui
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Zhang, Jie
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RESULT 10
US-10-125-237-5/c
US-10-125-237-5/c
; Sequence 5, Application US/10125237
; Publication No. US20030022329A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
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                                                                         LysAspLeuTyrAlaTrpAlaIleLeuThr 449
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APPLICANT: Drimanac, Radoje T.
TITLE OF INVENTION: No. US20030022329Alel Nucleic Aci
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 09/668,317
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 5
LENGTH: 2307
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (1612)..(2184)
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                                     TTCCGGAGAACAATCAGATTGAAGCTTATCTATGACAGATGTGATCTTAACTGTCGGATC
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Zhao, Qing A.
Xue, Aidong J.
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Drmanac, Radoj
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RESULT 11
US-09-816-828-9/c
US-09-816-828-9/c
; Sequence 9, Application US/09816828
; Patent No. US20020150898A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
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; NAME/KEY: CDS
; LOCATION: (1612)..(2211)
US-09-816-828-9
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020150898Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
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                            TTCCGGAGAACAATCAGATTGAAGCTTATCTATGACAGATGTGATCTTAACTGTCGGATC
                                                                                                                                  TACAATAAGCCTCATGAAGAGCCTTCCAACTCCCTCATGGCAATTGAATGTCGTGTCTGT
                                                                                {\tt GGAGATAAAGCTTCTGGATTTCACTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTC}
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Wang, Zhiwei
Zhao, Qing A.
Zhang, Jie
Wang, Jian-Rui
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Xue, Aidong
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Conservative:
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Sequence 1, Application US Patent No. US20020137665A1 GENERAL INFORMATION: APPLICANT: EVANS, Ronald
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TITLE OF INVENTION: MODULATORS OF PEROXISOME
TITLE OF INVENTION: RECEPTOR-GAMMA,
TITLE OF INVENTION: AND METHODS FOR THE USE
FILE REFERENCE: SALK1480-2
CURRENT APPLICATION NUMBER: US/10/142,373
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US/09/788,070
PRIOR APPLICATION NUMBER: US/09/788,070
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
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Best Local Similarity:
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; LOCATION: (352)..(1776)
US-10-142-373-1
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TYPE: DNA
ORGANISM: Mus Musculus
FEATURE:
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86.40%
85.36%
58.87%
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US-09-931-007A-1 (1-688) x US-10-142-373-1 (1-2005)
               ValGluProAlaSerProProTyrTyrSerGluLysThrGlnLeuTyrAsn------
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Matches:
Conservative:
Mismatches:
Indels:
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GENERAL INFORMATION:

APPLICANT: YOUNG, Paul
TITLE OF INVENTION: PROCess for Identifying
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,923
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US-09-954-456-554
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Score:
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; OTHER INFORMATION: n=a
US-09-954-456-554
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Best Local Similarity:
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SEQ ID NO 554
LENGTH: 3301
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FILING DATE: 2000-09-26
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APPLICATION NUMBER: US/60/235
FILING DATE: 2000-09-26
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                                                               AsnAspGlnValThrLeuLeuLysTyrGlyValHisGluIleIleTyrThrMetLeuAla
                                                                                                      ACCGTGCGGGAGCTCACTGAGTTCGCCAAGAGCATCCCCAGCTTCAGCAGCCTCTTCCTC
                                                                                                                    AlaValGlnGluIleThrGluTyrAlaLysSerIleProGlyPheValAsnLeuAspLeu
                                                                                                                                                          CCTCCCTACAAGGAGATCAGCGTGCACGTCTTCTACCGCTGCCAGTGCACCACAGTGGAG
                                                                                                                                                                       GluGlnSerLysGluValAlaIleArgIlePheGlnGlyCysGlnPheArgSerValGlu
                                                                                                                                                                                                                         ArgAlaLeuAlaLysHisLeuTyrAspSerTyrIleLysSerPheProLeuThrLysAla
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                                                    AACGACCAGGTTACCCTTCTCAAGTATGGCGTGCACGAGGCCATCTTCGCCATGCTGGCC
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APPLICANT: Philips, Russell
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
TITLE OF INVENTION: PROLIFERATOR-ACTIVATED RECEP
FILE REFERENCE: R-683
CURRENT APPLICATION NUMBER: US/10/013,807
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,916
PRIOR TILING DATE: 2000-12-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                        Pred. No.:
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LENGTH: 1323
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                Sequence 1855, Application Patent No. US20020131971A1 GENERAL INFORMATION:
                                                                                                          APPLICANT: King, Gordon E.
APPLICANT: Meagher, Maddeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
NUMBER OF SOFTWARE:
                                                   CURRENT FILING DATE: 2001-12-26
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| AAGGCCCGGAGCATCCTCACCGGCAAGTCCAGCCACCAACGCACCCTTTGTCATCCACGAC
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5
; OTHER INFORMATION: n = A
US-10-033-528-1855
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                                                                   CTCATATCCGAGGGCCAAGGCTTCATGACAAGGGAGTTTCTAAAGAGCCTGCGAAAGCCT 245
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